

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2002, 06:42:55 ; Search time 2040.31 Seconds
(without alignments)
13897.622 Million cell updates/sec

Title: US-09-664-840-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1337.4	98.7	1358	AF247133
2	351.6	25.9	1346	AY050838
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5	284.8	21.0	1156	D88537
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7	265.2	19.6	900	AF332434
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11	260	19.2	8	D49383
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ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE
1	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Limnanthes douglasii	1358 bp mRNA linear, PLN 02-NOV-2000						
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Douglas's meadowfoam.							
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Limnanthes douglasii							
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosoids II; Brassicales; Limnanthaceae; Limnanthes.							
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	1 (bases 1 to 1358)							
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Kloney,A.J.							
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Production of fatty acid components of meadowfoam oil in somatic soybean embryos							
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Plant Physiol. 124 (1), 243-252 (2000)							
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	10982439							
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	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Caboon,E.B.							
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Direct Submission							

AUTHORS	Yamada, K., Liu, S. X., Pham, P. K., Banb, J., Banno, F., Dale, J. M., Goldsmith, A. D., Jiang, P. X., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koeseema, E., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Nguyen, M., Palm, C. J., Sakurai, T., Sato, M., Seki, M., Shinozaki, K., Tracy, S. E., Shinozaki, K., Hayashizaki, Y. and Shinozaki, K.
TITLE	Direct Submission
JOURNAL	Submitted (08-AUG-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
COMMENT	RKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RFLV cDNAs (RFLV cDNA : "RKEN Arabidopsis Full-length cDNA") : Seki, M., Narusaka, M., Ishida, J., Sato, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
FEATURES	The Sak, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RFLV cDNAs: Yamada, K., Liu, S. X., Pham, P. K., Banb, J., Banno, F., Dale, J. M., Goldsmith, A. D., Jiang, P. X., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koeseema, E., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shin, P., Southwick, A., Tracy, S. E., Davis, R. W., Ecker, J. R. and Theologis, A.
SOURCE	Yamada, K. (SSP/PGEC) and Seki, M. (RKEN GSC) contributed equally to this work. Shinozaki, K. (RKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
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 REFERENCE 1 (bases 1 to 918)
 Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Egu, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
 Full length cDNA of gene T21E18.13 (GI:8810470)
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 918)
 REFERENCE Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Egu, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
 JOURNAL Direct Submission
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 REFERENCE 1 (bases 1 to 1178)
 Tasaka, Y.
 TITLE Direct Submission
 JOURNAL Submitted (24-OCT-1996) Yasushi Tasaka, National Institute for Basic Biology, Department of Regulation Biology, 38 Nishigonaka, Myodaijicho, Okazaki, Aichi 444, Japan (E-mail:tasakay@nibb.ac.jp, Tel:+81-564-55-7602, Fax:+81-564-54-4866)
 REFERENCE 2 (sites)
 Qy 2 Fukuchi-Mizutani, M., Tasaka, Y., Tanaka, Y., Ashikari, T., Kusumi, T. and Murata, N.
 TITLE Characterization of delta 9 acyl-lipid desaturase homologues from Arabidopsis thaliana
 JOURNAL Plant Cell Physiol. 39 (2), 247-253 (1998)
 MEDLINE 98220322
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AUTHORS	Tasaka, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-OCT-1996) Yasushi Tasaka, National Institute for Basic Biology, Department of Regulation Biology; 38 Nishigonaka, Myodaijicho, Okazaki, Aichi 444, Japan (E-mail:tasakayen@nib.ac.jp, Tel: +81-564-55-7602, Fax: +81-564-54-4866)		
REFERENCE	2 (sites)		
AUTHORS	Fukuchi-Mizutani, M., Tasaka, Y., Tanaka, Y., Ashikari, T., Kusumi, T. and Murata, N.		
TITLE	Characterization of delta 9 acyl-11lipid desaturase homologues from Arabidopsis thaliana		
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Oy 849 ggaagttattaccaccaacataatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 908
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Oy 909 aacaaccacacacacacacacacacacacacacacacacacacacacacacacacacac 968
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Db 906 CCAACGAGAGCTCA 919

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RESULT 6
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LOCUS Arabidopsis thaliana putative delta 9 desaturase
DEFINITION (728P16.15/At2g31360) mRNA, complete cds.
ACCESSION AY045918
VERSION AY045918.1 GI:15028190
KEYWORDS FLI CDNA.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1253)
Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Dale, J.M., Goldsmith, A.D.,
Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P.,
Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,
Karlín-Neumann, G., Kawai, J., Kim, C., Kosemura, E., Lam, B., Lin, J.,
Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Tracy, S.E.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

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TITLE
JOURNAL
REFERENCE
AUTHORS
Full Length cDNA of gene T28P16.15/At2g31360 (GI:4589964)
Unpublished
2 (bases 1 to 1253)
Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Dale, J.M., Goldsmith, A.D.,
Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P.,
Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,
Karlín-Neumann, G., Kawai, J., Kim, C., Kosemura, E., Lam, B., Lin, J.,
Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Tracy, S.E.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Direct Submission
Submitted (09-JUL-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu, S.X.,
Pham, P.K., Banh, J., Dale, J.M., Goldsmith, A.D., Jiang, P.X.,
Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M.,
Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T.,
Karlín-Neumann, G., Kim, C., Kosemura, E., Lam, B., Lin, J., Meyers, M.C.,
Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A.,
Tracy, S.E., Davis, R.W., Ecker, J.R. and Theologis, A.
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC)
contributed equally to this work as PIs.
FEATURES
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location/Qualifiers
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db_xref="taxon:3702"
chromosome="2"
clone="RAF105-09-K18 (R10113)"
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GRANVEDLKRWFYRFLQKTVLEHIGLDFLEFVLCGMFVFMGVGAALAEVHC
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Db	226	CCGTTTTATTTCACATGGCTGCCTCTTTGGGTACGTTTTTGTT-----TTACACCATTC	279
Oy	369	gggttctctgtatcatcactttgtcttcataagtgtgtcttaactatgycggtttcaagctt	428
Db	280	GGTGGTCTTGGTATCACCGTCTCTATCATGCAACTGGGTACCGGAGTTTAAAGTC	339
Oy	429	cctaagtctgtgtgtgtacttcttcgcctactgtgtgcctctcgcctctcaaggagaacc	488
Db	340	CCTTAATGGCTTTGAGTATCTCTTAGCCTATTTGTGCCCCCTTCTCGCTATTCAAGGAGATCCG	399
Oy	489	atggaaatggtgaaacaacatalagglacccaaccagtlcgtcgaalacagaagaagatgt	548
Db	400	ATTGATTGGGTGAGTACACATCGTTTACCATACACAGCTTCACGGATVTCAGAACGGTATCCA	459
Oy	549	catgtctcaactcaaagaeatttgctctgtcacatatgtgtgtgtctctgtcaagaattta	608
Db	460	CATAGTCTCTAAGGAAGGTTTTTGGTTTGGTATCTCTTCTTGGAATCTAAGACTCTGCCAT	519
Oy	609	tctgcgcgaaaaacgtgtgtgagcgcgaagaagaacatgtgaatlgttatgaagaacaagcctc	668
Db	520	CTTGTTTCAAAGGTGGA---AGAAAGACCAAACTGTGAGCATTTTGAAGACGCATATGTTTT	576
Oy	669	tacagatcccctccgaagaacctatagtfaccaatcaatltgtcgtctaatagctctacttac	728
Db	577	TATAGCTTCTTTCAAGAAAACAGTGTCTATTTCACATTTTAGAGTTGGGTTCTCTTCTCTTC	636
Oy	729	tacgtcgaagggtttccatacatgtctcgtggaatvggtttcagaattgtttaatgttc	788
Db	637	TACCTTGGTGGCATGTCCTTCTGTTACTTGGGGAAVTGGGGAGCAGCATTTGGAAATG	696
Oy	789	cattccactcttcgcataaacatcagttgttataaabaagggcgaagccatgtgaatct	848
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Oy	849	ggaagatllatacgaaccaacaataatgttttgcatgtgtgcgtttggaagagcctygcat	908
Db	757	AATGACACTTCTCCGTAATCTTTGGTGTTATTCGGTATTTTCATTTGAGAGAGTGGCAGC	816
Oy	909	aacaacacacacgcacatcgaacaacatcagctcgcgaacggcgtagaaatgtgtgcagaatcga	968
Db	817	AACATTCATCATGCTGTGAGTCAAGCTGACGAAGCACTGTAATGGTGGCACAATAAGAC	876
Oy	969	gttaactgtgtacgttatacgaagacttacaagcataatgtgatgtgtgtcaccaaatgtgaagcta	1028
Db	877	ATTTTCGTGGTACATTTGTTTCGGTTTTGCATAAATATTCGGTTTAAAGCAGCATGTGAAATGTG	936
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DEFINITION	Arabidopsis thaliana putative desaturase protein (T21E18.17) mRNA,		
complete cds.			
ACCESSION	AF332434		
VERSION	AF332434.1	GI:12083275	
KEYWORDS	FLI cDNA.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsida.		
	1 (bases 1 to 900)		
	Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P.,		
	Lee,J.M., Tortum,M., Yu,G., Brooks,S., Chao,Q., Chen,H.,		
	Kastlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,		
REFERENCE			
AUTHORS			

TITLE	Palm,C.J., Shim,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
JOURNAL REFERENCE	Full Length cDNA of gene T2IE18.17 (GI:8810474)
AUTHORS	2 (bases 1 to 900) Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P., Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H., Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shim,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE	Direct Submissions
JOURNAL	Submitted (28-DEC-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
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Query Match	19.6% Score 265.2; DB 8; Length 900;
Best Local Similarity	58.9%; Pred. NO.1.3e-61;
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OY	628 gccgaagaacaacatgtgaatgatttgaagaagaacagccttctacagattcctccagaana 687

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RESULT 8
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 LOCUS Rose hybrida mRNA for delta-9 desaturase homologue, R44.
 DEFINITION D49384
 ACCESSION D49384
 VERSION D49384.1 GI:2580426
 KEYWORDS Delta-9 desaturase.
 SOURCE Rosa hybrida (strain:Kardinal) Senescence Petal cDNA to mRNA, clone.lib:lamda ZAPII clone:RP44.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Rosoidae; Rosa.
 REFERENCE 1 (bases 1 to 1153)
 AUTHORS Nishida,I.
 TITLE Direct Submission
 JOURNAL Submitted (16-FEB-1995) Ikuro Nishida, National Institute for Basic Biology, Cellular Regulation; 38 Nishigonaka, Myodaiji-cho, Okazaki, Aichi 444, Japan (E-mail:nishida@nibb.ac.jp, Tel:0564-55-7602, Fax:0564-54-4866)
 2 (sites)
 REFERENCE 2 (sites)
 AUTHORS Fukuchi-Mizutani,M., Savin,K., Cornish,E., Tanaka,Y., Ashikari,T., Kusumi,T. and Murata,N.
 TITLE Senescence-induced expression of a homologue of delta 9 desaturase in rose petals
 JOURNAL Plant Mol. Biol. 29 (4), 627-635 (1995)
 MEDLINE 96128006
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RESULT 9
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DEFINITION Rose hybrida mRNA for delta-9 desaturase homologue, RP46.
ACCESSION D49385
VERSION D49385.1 GI:2580428
KEYWORDS Delta-9 desaturase.
SOURCE Rosa hybrida (strain:Kardinal) Senescence Petal cDNA to mRNA,
clone_11b:Lambda ZAPII clone:RP46.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1 (bases 1 to 1126)
AUTHORS Nishida,I.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-1995) Ikuo Nishida, National Institute for Basic
Biology, Cellular Regulation; 38 Nishigonaka, Myodaiji-cho,
Okazaki, Aichi 444, Japan (E-mail:nishidaenibb.ac.jp,
Tel:0564-55-7602, Fax:0564-54-4866)
2 (bases 1 to 1126)
REFERENCE Fukuchi-Mizutani,M., Savin,K., Cornish,E., Tanaka,Y., Ashikari,T.,
AUTHORS Kusumi,T. and Murata,N.
TITLE Senescence-induced expression of a homologue of delta 9 desaturase
JOURNAL In rose petals
MEDLINE Plant Mol. Biol. 29 (4), 627-635 (1995)
FEATURES
SOURCE 96128006
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Query Match 19.2%; Score 260; DB 8; Length 1126;
Best Local Similarity 59.0%; Pred. No. 3.5e-60;
Matches 487; Conservative 0; Mismatches 330; Indels 9; Gaps 2;

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QY 527 cgtcgatcacgaagaagatgtctacagtcacacccaagaatttggtctgcacatg 586
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Rosidae; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1 (bases 1 to 1126)
AUTHORS Fukuchi-Mizutani,M., Savin,K., Cornish,E., Tanaka,Y., Ashikari,T.,
Kusumi,T. and Murata,N.
TITLE Senescence-induced expression of a homologue of delta 9 desaturase
JOURNAL In rose petals
MEDLINE Plant Mol. Biol. 29 (4), 627-635 (1995)
REMARK GenBank staff at the National Library of Medicine created this
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AUTHORS	Murata,N.		
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ID AAC39176 standard; DNA; 1359 BP.

AC AAC39176

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 23656

KW Hybridisation assay; genetic mapping; gene expression control;

metabolic pathway; promoter; termination sequence; ss

OS *Arabidopsis thaliana*.

PN EP1033405-A2

06-SEP-2000 . PD

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XX AAC38595;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 21544.

XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EPI033405-A2.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000BP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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Query Match 19.3%; Score 261.2; DB 21; Length 1125;

Best Local Similarity 58.5%; Pred. No. 5e-65;

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Matches 496; Conservative 0; Mismatches 343; Indels 9; Gaps 2;

QY 204 ggtgtggaagaagaatccaaagagattcggcgccggaatggaacccctcgtgatataa 263
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DB 75 gcggtcgctgggggaaagaagcattatttttcggaatggaacccggtatgagc 134
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QY 264 aacgcgcgtcaattactggtctcgtcgtcttcgaagcgtgagcccttatttcagc 323
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DB 135 agagcttcggctgtggggcgctgacatactgtctgtgtggtcgcgttaataa 194
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QY 324 tgggaatcggttttgatctcttatactgtgtgtgttcggaagcggtgtctgtatc 383
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 195 tgggaagctcccgctcggtgtgattctcgtctagtagtagtagtagtagtagtag 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 384 accttgcgtccataggtgtcttactcaatgaggtttcaagcttcttaagttgtag 443
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB 489 ggaag---gagctgacaaagtgatgagacttgaagcaacaatggtctctatagttcttcoga 545
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DB 606 ccttaacctacttgcgcgtgtgtgtgtgggaacaaatcgtttacaatggaacttgcctc 665
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 666 ataactcgcgtatgcataatttgggtgtcgtcgagcatggaacacataagcacctctcgt 725
QY 864 aacataatgtttgttgcatttgcgttttggaaaggctctgcataacacacacacgca 923
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB 786 ttgaagccttcgcgcaggaagcaggaactggaatgatacaggttagacttaacttggtaacc 845
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB 906 aagcgaaa 913

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RESULT 10

AAC39817 standard; DNA; 1150 BP.

AAC39817;

17-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 26011.

Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KM metabolic pathway; promoter; termination sequence; ss.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

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PF 25-FEB-2000; 2000EP-0301439.
XX XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126284.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
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XX 19-APR-1999; 99US-0130077.
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PR 29-OCT-1999; 99US-0162142.

Query Match	18.0%;	Score 243.4;	DB 21;	Length 1150;
Best Local Similarity	57.1%;	Pred. No. 6.9e-60;		
Matches 486;	Conservative 0;	Mismatches 356;	Indels 9;	Gaps 2

[illegible]

RESULT 11

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AC AAC39174;	
XX	
DT 17-OCT-2000 (first entry)	
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 23649.	
XX	
KW Hybridisation assay; genetic mapping; gene expression control,	
KM protein identification; signal transduction pathway;	
KV metabolic pathway; promoter; termination sequence; ss.	
XX	
OS Arabidopsis thaliana.	
XX	
PN EP1033405-A2.	
XX	
PD 06-SEP-2000.	
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PF 25-FEB-2000; 200EP-0301439.	
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RESULT 12
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ID AA093132 standard; DNA: 819 BP.
XX
AC AA093132;
XX
DT 06-MAR-1996 (first entry)
XX
DE Anabaena variabilis delta-9 desaturase gene.
XX
KW Anabaena variabilis; delta-9 desaturase; delta-12 desaturase; probe;
KM Synecococcus; fatty acid; plant; resistance; low temperature; ds.
XX
OS Anabaena variabilis.
XX
FH Key Location/Qualifiers
FT misc_difference 82..84
FT /tag= a
FT /trans_except= seq: TTT, a.a.: Pha (s1c)
XX
PN JF07170985-A.

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XX 11-JUL-1995.
PD
XX 22-SEP-1993; 93JP-0236719.
PF
XX 22-SEP-1993; 93JP-0236719.
PR
XX (MITU ) MITSUBISHI CHEM CORP.
PA (MITS ) MITSUBISHI CORP.
PA (TOEL ) TOHOKU ELECTRIC POWER CO.
XX
XX WPI: 1995-271456/36.
DR P-PSDB; AAR76811.
XX
PT New gene encoding delta9 desaturase isolated from Anabaena
PT variabilis - useful for improving the fatty acid compsn. of plants,
PT and increasing resistance to low temperatures.
XX
PS Claim 1; Page 4-5; 5pp: Japanese.
XX
CC The nucleotide sequence of the novel isolated Anabaena variabilis delta-9
CC desaturase gene. The gene was isolated from an Anabaena genomic library
CC in lambda-DASH II by plaque hybridisation using a 1.1 kb HincII fragment
CC of the Synecocystis PCC 6803 delta-12 desaturase gene as a probe. The
CC probe isolated a 2.1 kb fragment which in turn hybridised to a 7 kb
CC fragment in a genomic Southern blot. This fragment was cloned into the
CC vector pUC303 to produce pUC303/7-Kb, and used to transform Synecococcus
CC PCC 7942. The transformant contained 18 of 18:2 fatty acid upon
CC expression of the gene. The gene may also be used to transform plants to
CC alter their fatty acid compositions and to increase the resistance of
CC plants to low temps.
XX
SQ Sequence 819 BP; 182 A; 181 C; 190 G; 266 T; 0 other;

Query Match 14.0%; Score 189.4; DB 16; Length 819;
Best Local Similarity 55.2%; Pred.No.2;je-44;
Matches 417; Conservative 0; Mismatches 326; Indels 12; Gaps 2;

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Db 193 caccgcagtttccagactcccaagctggttgaataatttctcagtgcttgcgggaactc 252
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DT	22-SEP-1995	(first entry)	
DE	Delta-9-desaturase desC gene.		
KW	Delta-9-desaturase; desC gene; cyanobacterium; cold tolerance;		
KW	fatty acid; stearic acid; oleic acid; ds.		
OS	Anabaena variabilis.		
XX	Key	Location/Qualifiers	
FT	CDS	1..819	
FT		/+tag- a	
XX	EP644263-A.		
XX	22-MAR-1995.		
XX	22-SEP-1994;	94EP-0114957.	
XX	22-SEP-1993;	93JP-0236720.	
XX	(MORA/) MURATA N.		
XX	(MITU) MITSUBISHI CHEM IND LTD.		
XX	(MITS) MITSUBISHI CHEM.		
XX	(TOEL) TOHOKU ELECTRIC POWER CO.		
XX	Murata N;		
XX	WPI; 1995-116988/16.		
XX	P-PSDB; AAR70260.		
XX	New isolated gene encoding delta 9 desaturase of cyanobacteria		
XX	useful for transforming plants, animals or microorganisms to		
XX	improve low temp. tolerance		
XX	Disclosure; Page 10-11; 14pp; English.		
XX	Genomic DNA of Anabaena variabilis M-3 was screened with a fragment		
XX	of the delta-12-desaturase gene (desA) of Synechocystis PCC6803 as		
XX	probe, and the Anabaena desa gene was isolated. A new ORF located		
XX	upstream of this desa gene was identified as the delta-9-desaturase		
XX	gene (desC).		
XX	Sequence 819 BP; 182 A; 181 C; 190 G; 266 T; 0 other;		
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ALIGNMENTS

RESULT 1
US-08-309-182B-2
Sequence 2, Application US/08309182B
Patent No. 5639645
GENERAL INFORMATION:
APPLICANT: No. 563964510 MURATA
TITLE OF INVENTION: A RECOMBINANT 9 DESATURASE AND A GENE
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 Inch, 500 kb
OPERATING SYSTEM: IBM Compatible
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,182B
FILING DATE: September 20, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORGANISM: Anabaena variabilis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..816
IDENTIFICATION METHOD: P
US-08-309-182B-2


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1 NAME: Warren M. Cheek, Jr.
2 REGISTRATION NUMBER: 33,367
3 REFERENCE/DOCKET NUMBER:
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 202-371-8850
6 TELEFAX: 202-371-8856
7
8 INFORMATION FOR SEQ ID NO: 7:
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10 SEQUENCE CHARACTERISTICS:
11     LENGTH: 1355 base pairs
12     TYPE: nucleic acid
13     STRANDEDNESS: double
14     TOPOLOGY: linear
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16 MOLECULE TYPE: cDNA to mRNA
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18 HYPOTHETICAL:
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20 ANTI-SENSE:
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22 FRAGMENT TYPE:
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24 ORIGINAL SOURCE:
25     ORGANISM: Candida albicans
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27 STRAIN:
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72     AUTHORS:
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74     TITLE:
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76     JOURNAL:
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78     VOLUME:
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80     ISSUE:
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TITLE OF INVENTION: REPEAT DNA MARKERS
 NUMBER OF SEQUENCES: 147
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Promega Corporation
 STREET: 2800 Woods Hollow Road
 City: Madison
 STATE: Wisconsin
 COUNTRY: U.S.A.
 ZIP: 53711-5399
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
 COMPUTER: IBM compatible PC
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Word 97 (DOS text format)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/018,584A
 FILING DATE: 04-Feb-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Grady J. Prentchick
 REGISTRATION NUMBER: 29,018
 REFERENCE/DOCKET NUMBER: 16026.9180
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 257-3501
 TELEFAX: (608) 257-2275
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 bp
 TYPE: Nucleic Acid
 STRANDEDNESS: Double
 TOPOLOGY: Circular
 MOLECULE TYPE: Genomic DNA
 HYPOTHETICAL: no
 IMMEDIATE SOURCE:
 LIBRARY: plasmid, pGem3Zf(+)
 CLONE: G132
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 4 qter
 US-09-018-584A-13

[illegible]

Search completed: September 13, 2002, 08:46:55
Job time: 7345 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2002, 06:38:55 ; Search time 1767.26 Seconds
(without alignments)
10348.434 Million cell updates/sec

Title: US-09-664-840-1
Perfect score: 1355
Sequence: 1 gcttgagactctctctac.....ttgtgtcctcaaaaaaaaaa 1355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estsdb:
2: em_estsdb:
3: em_estsdb:
4: em_estsdb:
5: em_estsdb:
6: em_estsdb:
7: em_estsdb:
8: em_estsdb:
9: em_estsdb:
10: em_estsdb:
11: em_estsdb:
12: em_estsdb:
13: em_estsdb:
14: em_estsdb:
15: em_estsdb:
16: em_estsdb:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	259.2	19.1	590	10	BF053048 EST438278
2	203.6	15.0	503	10	BE802366 sr29b07.y
3	181.6	13.4	528	10	BE919440 EST23125
4	179.4	13.2	564	9	AV439619
5	171.6	12.7	691	10	BJ167260
6	167.6	12.4	556	9	AV442617
7	160.8	11.9	552	9	AV551184
8	155.4	11.5	680	10	BJ171184
9	152.8	11.3	513	9	AV550066
10	152.4	11.2	629	9	AV550066
11	142.4	10.5	494	9	AT993202
12	142.2	10.5	494	9	AT993202
13	142	10.5	700	10	BI933998
14	142	10.5	721	10	BI933998
15	141.8	10.5	660	10	BI933998
16	139.4	10.3	458	9	AV554343
17	139	10.3	520	9	AV554343

18	138	10.2	701	9	AT483228
19	129.6	9.6	598	9	AV539911
20	128.8	9.5	428	10	BI720501
21	126.2	9.3	313	9	AT178264
22	124.4	9.2	592	9	AV539024
23	123.2	9.1	492	9	AV544942
24	122.6	9.0	389	10	T46147
25	122	9.0	447	9	AT992605
26	121.6	9.0	281	9	AT178263
27	118.8	8.8	600	9	AV539795
28	117.6	8.7	600	9	AV538469
29	114.8	8.5	523	9	AV538985
30	114.8	8.5	536	9	AV542250
31	113.6	8.4	540	9	AA041026
32	113.4	8.4	395	10	T20690
33	111.6	8.2	602	9	AV538452
34	106.6	7.9	479	9	AV539783
35	97.6	7.2	341	10	Z30751
36	94.6	7.0	375	9	AV551324
37	93.2	6.9	784	12	BH578290
38	92.8	6.8	501	9	AV539361
39	92	6.8	615	9	AT483237
40	87.2	6.4	720	12	BH438059
41	86.8	6.4	522	10	N97264
42	86.4	6.4	406	9	AV539450
43	85.6	6.3	412	9	AV539469
44	81.2	6.0	663	10	BG129876
45	81	6.0	418	10	Z32595

ALIGNMENTS

RESULT 1
LOCUS BF053048 590 bp mRNA linear EST 16-OCT-2000
DEFINITION EST438278 potato leaves and petioles Solanum tuberosum cDNA clone
CST34E7 5' sequence, mRNA sequence.
ACCESSION BF053048
VERSION BF053048.1 GI:10806944
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 590)
van der Hoeven R.S., Bezzerides J., Holt, I.E., Liang, F., Cho, J.,
Uttarback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning
, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: Please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
1..590
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="CST34E7"
/clone_1db="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Tissue was supplied by Dr. Fry (Cornell University).
leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."

FEATURES

source

BASE COUNT

152 a 112 c 152 g 174 t

Db 427 TATATGACGAGGAGGATTTCTTCTTGTATGAGGAAATGGAGATGAGATTG 480

RESULT 3

BE919440

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

322; Conservative

0; Mismatches

194; Indels

4; Gaps

2;

327

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Db 309 TGGGAAGCCAAACATGTGGGGGATTTGGAGACGAGTTTATATCATCTTATCGTGA 368

RESULT 4

AV439619/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

267; Conservative

0; Mismatches

146; Indels

0; Gaps

0;

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564

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504

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JOURNAL COMMENT

Unpublished (2002)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified IPS phage vector (No bi Rec, Germany). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.

FEATURES

source

1. 680
/organism="Physcomitrella patens subsp. patens"
/db_xref="taxon:145481"
/clone="pPh28c15"
/clone_lib="full length cDNA library, chloronemata and young gametophores"
/tissue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"
BASE COUNT 150 a 246 c 122 g 162 t
ORIGIN

Query Match 11.5%; Score 155.4; DB 10; Length 680;
Best Local Similarity 66.0%; Pred. No. 4.8e-25;
Matches 225; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 724 tttaacgctgcgaggtttccatcatgtctcgtgggaattggttttagattggttta 783
Db 668 tctatgccgtggagagatttccctacatcgtctggggcatgctgtgagcagctgtggg 609
Qy 784 ttttcattccactcttcgtatcatcagctggttcataaataagggcggaagccatgga 843
Db 608 tctatccatccatcagctgtttgtaacttgcattccatcgtctggggatccgcaaaagtga 549
Qy 844 atactggaattatcgaacaaataltgtttgtcattgtcgtttggaagaaggtc 903
Db 548 acacgggaacattgtctcggaacaaactggtggctgcatgttgcgatttggggaagcgt 489
Qy 904 ggcataaacaacacacgcatcgaacatcagctcgaacagggctagaatgtgtcaga 963
Db 488 ggcacaaacacacacgcatcgaacatcagctcgaacagggctagaatgtgtcaga 429
Qy 964 tctgatttactgtgtaactatcgaacatcgaacatcgaacatcgaacatcgaacatcga 1023
Db 428 tggaccggacatgt 369
Qy 1024 agctaccactgaagctcagaagcaaaagctcaagaagaag 1064
Db 368 agctaccggagagatcagatcgagaaagctgcatattcaag 328

RESULT 9

AV550066 513 bp mRNA linear EST 06-SEP-2000
LOCUS AV550066 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
DEFINITION cDNA clone R2107g08R 5', mRNA sequence.
ACCESSION AV550066
VERSION AV550066.1 GI:8721479
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 513)
Asamizu, E., Nakamura, Y., Sato, S., and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

TITLE

size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)

JOURNAL MEDLINE COMMENT

Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

source

1. 513
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="R2107g08R"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 121 a 104 c 130 g 158 t
ORIGIN

Query Match 11.3%; Score 152.8; DB 9; Length 513;
Best Local Similarity 60.4%; Pred. No. 1.9e-24;
Matches 272; Conservative 0; Mismatches 172; Indels 6; Gaps 1;

Qy 189 cggacatcagaagtcgtgttgagagaaatccaaagatcttgcgcggaatggaac 248
Db 66 cccggcggcggcgagagaaagagagagatgggtttggatgagagagagagagagag 125
Qy 249 cctcgtgattatcaaaacgcgcctcattcgtgtcctcgtcgtcgtcgtcgtcgtcgtcgt 308
Db 126 agattagattatgcaatttctcagcttcttctcagcttctcgtcgtcgtcgtcgtcgtcgt 185
Qy 309 ccccttattcagctgagatgctgttgatcctccttattccttctgtgttctgcgaagc 368
Db 186 ccgttt 239
Qy 369 ggtgtctgtgtatcacttctgtcctcagtaggaggtcctcagtaggaggtcctcagtagg 428
Db 240 ggtgtgtgtgtatcacttctgtcctcagtaggaggtcctcagtaggaggtcctcagtagg 299
Qy 429 cctaagttgtgtgacttcttctcactcgtgtcctcgtcgtcgtcgtcgtcgtcgtcgtcgt 488
Db 300 ccttaattggtgacttcttctcactcgtgtcctcgtcgtcgtcgtcgtcgtcgtcgtcgt 359
Qy 489 atggaatggtgtgagcaacatagatgacatccacaggtcgtcgtcgtcgtcgtcgtcgtcgt 548
Db 360 attgattgggtgagcaacatagatgacatccacaggtcgtcgtcgtcgtcgtcgtcgtcgt 419
Qy 549 catagtcacactcagaagatttggctcgtcagatgttggctcgtcagatgttggctcgtcag 608
Db 420 catagtcctcagaagatttggctcgtcagatgttggctcgtcagatgttggctcgtcag 479
Qy 609 ttctgcgaanaacgt 638
Db 480 ctgtgtttcnaagtggaagagacaaac 509

RESULT 10

AV440963 629 bp mRNA linear EST 14-NOV-2000
LOCUS AV440963 Arabidopsis thaliana above-ground organ two to six-week
DEFINITION old Arabidopsis thaliana cDNA clone AP217b08_f 3', mRNA sequence.
ACCESSION AV440963
VERSION AV440963.1 GI:7611340
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE	AUTHORS	TITLE
JOURNAL MEDLINE COMMENT	CONTACT: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/. Location/Qualifiers	1. 629 /organism="Arabidopsis thaliana" /strain="Columbia" /db_xref="taxon:3702" /clone="AP217b08_f" /clone_lib="Arabidopsis thaliana above-ground organ two to six-week old" /tissue_type="aboveground organs" /dev_stage="two to six-week old" /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT	210 a 159 c 99 g 161 t	
ORIGIN		
Query Match	11.2%; Score 152.4; DB 9; Length 629;	
Best Local Similarity	60.3%; Pred. No. 2,36-24;	
Matches	252; Conservative 0; Mismatches 166; Indels 0; Gaps 0;	
635	gtggccgaagaacaatgtgaatgatttgaagaacaagccttctacagatccctccaga	684
601	gtggagaaagacaaacgtgagatttgaaagacgaattgttatagtttcttccaga	542
685	aacctatagtacacataatgagctcctaatagcctccttaccagtcggagaggttc	744
541	aaacagctcatatttcacatttttagattggcttcttcttcttcttccacgttgacatgt	482
745	catcatctgctcgggaaatggatttagatggtgtgttcatgttccatccacttcgcta	804
481	ctttcgttaccttgccgaatggggagagacagacatttggaatgcacgacttgcctca	422
805	tcaactcagttgtcatataatgagcgggaagccatgtgaatctatgtgaattatcgaca	864
421	taaatctactctgccaattttggggcactcgaaatttgaaagccaaatcacatttctgta	362
865	acaatatttctgtgcatctgtgcttcttggaagagctgtgcataacaacaccacgcat	924
361	atgttttgatggatttgcggtatttttcatttttgagagacagttggcacaaatcatcatgct	302
925	tcgaaacaatcagctcgcagacagggctagaatggtgagatcgatctgattgtagctta	984
301	tgcagctcatcggcttagacaaagaccttggaatgctggccaatagacatttccgtgacattg	242
985	tcagagctctacaagctattgagctgtgacaaatggaagctcaagctcaagctcaagctta	1042
241	tttcggtttttcgaaatttttcggttttagccgaccgatgtgaatgtcccaacggagcctca	184
RESULT 11		
AV550487	522 bp mRNA linear EST 06-SEP-2000	
LOCUS	AV550487 Arabidopsis thaliana roots Columbia Arabidopsis thaliana	
DEFINITION	cDNA clone K113b04R 5', mRNA sequence.	
ACCESSION	AV550487	
VERSION	AV550487.1 GI:8721900	
KEYWORDS	EST.	
SOURCE	thale cress.	

ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
AUTHORS	Asamizu E., Nakamura Y., Sato S. and Tabata S.
TITLE	A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and site-selected cDNA libraries
JOURNAL MEDLINE	DNA Res. 7, 175-180 (2000)
COMMENT	Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/ Location/Qualifiers
FEATURES	1..522
source	/organism="Arabidopsis thaliana" /strain="Columbia" /db_xref="taxon:3702" /clone="R2113B04r" /clone_lib="Arabidopsis thaliana roots Columbia" /lisse_type="roots" /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT	127 a 103 c 134 g 158 t
ORIGIN	
Query Match	11.2%; Score 152.2; DB: 9; Length 522;
Best Local Similarity	61.1%; Pred. No 2.5e-24;
Matches	266; Conservative 0; Mismatches 163; Indels 6; Gaps 1;
OY	204 gtgttgagaggaaatccaaagaattctgacgcgaagaatggaaacctcgtatatacca 263
Db	90 GAGAAAGAAGAGACGAGATGGGTGTTGGATAGAAAGTGAAGAGATTAATATTATG 149
OY	264 aagcgcgacacttactcgtcgtcatgctcttcgaagagatggcgccctttattaccg 323
Db	150 AATATCTCAAGCTCTTTCACTGTATATTCCTCTCTCTTGCGCCGTTTTATTTCACT 209
OY	324 tggagatcgatttgatctcttaactctgcttgattctcgcaagsgtgatcttgatlc 383
Db	210 TGGTGGCGCTTTGGGCTTACGTTTTGTT-----TTACACCATGGGTGCTTGGTATC 263
OY	384 acttgtctcccaagatgctcttaactaatggcggatttcaaagtccctaagttgtag 443
Db	264 ACCGCTCTTATCAATCGGAACCTTGCTCAACCGAATTTCCMAAGTCCATAAAGGCTTNG 323
OY	444 tactcttgcactactggtcgtctctcgtctcttcgaagagatccgatggaaatggctgac 503
Db	324 TATCTCTTACCTTATTTGTCCTTCCCTTCCGCTATTTCAGGAGATCCCATTTGATGGTGAT 383
OY	504 aaecatagatcacaccacgaatctgcgatatagaaaagatgltcatagtlcaactcaa 563
Db	384 ACACATCGCTTACCATCACACAGATTCCAGGATTCAGAAAGCATGCACATAGTCTTAAGMA 443
OY	564 ggatttgcctcgtcacatcattggttggttctcttcgcaagaatttatctgctgaaaaagt 623
Db	444 GGTTTGGTTTAGTCATCTTCTTGGATCTATGACTCTGCTATCTTGTTCMAAAGTGT 503
OY	624 gttgcccgaagaac 638
Db	504 GGAAGAAGACAAC 518
RESULT 12	
LLOCUS	AI1993202
DEFINITION	AI1993202 494 bp mRNA linear EST 08-SEP-1999
CDNA CLONE	701495686 A. thaliana, Ohio State clone set Arabidopsis thaliana
ACCESSION	AT1993202
CDNA CLONE	701495686, mRNA sequence.

VERSION	AT1993202.1 GI:5840107		
KEYWORDS	EST.		
SOURCE	thale cress		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 494)		
ATTNORS	Chen J., Montlyana, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Giegler, K., Kim, C., Doyle, M., Brzoka, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, P., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.		
TITLE	Arabidopsis thaliana Gene Expression Microarray		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: David Smoller, Ph.D. Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc. 4633 World Parkway Circle, St. Louis, MO 63134, USA Tel: 877-577-2733 Fax: 314-427-3324 Email: servloce@genomesystems.com.		
FEATURES	Location/Dualifiers		
SOURCE	1..494 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /clone="701495686" /clone.lib="A. thaliana, Ohio State clone set" /note="cDNA library was made from selected clones from the Arabidopsis thaliana Ohio State clone set."		
BASE COUNT	127 a 108 c 108 g 151 t		
ORIGIN			
Query Match	10.5%: Score 142.4; DB 9; Length 494;		
Best Local Similarity	60.6%: Pred. No. 4.3e-22;		
Matches 269; Conservative	0; Mismatches 171; Indels 4; Gaps 2;		
QY 374	tccttgatcacttcttgctccataggtgtcttctacatcgtgcyggttccaagcttccctaa	433	
Db 49	TCCTTAGCTATCAATTTTCATACAGAGAACCTTGACCTCAAGACCTTAAAGCTTCCTAA	108	
QY 434	gttggttgatctcttcttgcctactgtgtgctctctgcctcttcagggagatcccatgga	493	
Db 109	ATGGCTTAAATATCCATTGCGCTATTTCCCTTTTCGCGCTTCAGGGTTCATCCAAATGA	168	
QY 494	atgtgtgacacacatagatgacatccaccacagctctgtcgatatacagaagaagatgttccatag	553	
Db 169	TTGGGTGATGACACATAGAGTTCACACACAGTTCACAAATTCAGACCGTGACCCACATAG	228	
QY 554	ttcaactcaaggatcttgctctgtcacatcgttgggttcttgcaaaagattatcgt	613	
Db 229	TCCATATCGAAGATTTCTGTTGTCAGACGTCCTTTTGGATTTTCAGACACACAGTTACATCAG	288	
QY 614	cgaaanaagctgtgtgcgaagaanaaagatgtaataatttggaagaanaagccttccatag	673	
Db 289	AGAAAAGTGTGAG---GACGTGACAACTGATGACTTGAAGCAACAATGTTTATAG	345	
QY 674	atctctccagaanaactatagtacatcaatcttgctcttaataagcttacttactagct	733	
Db 346	GTTCCTTCGAAACACAAATGGTGTCTCCACATCTTAACATTTTGGACCCCTGCTATTTATTT	405	
QY 734	cgagggagtttccatcatctgtctgagggaatggttttgattggtttagtcttccatc	793	
Db 406	GGGGGTCTACCTTAC---TAACTTTCGGCGTGGGTGTGGAGGAAAAATCGGTTACAAAGG	464	
QY 794	cacttcgctatacactcagttg 817		
Db 465	GACCTTGCCCATTAACCTGCGCATG 488		
RESULT	13		

BI933998	LOCUS	BI933998	700 bp	mRNA	linear	EST 18-OCT-2001
	DEFINITION	EST553887 tomato flower, anthesis Lycopersicon esculentum cDNA				
	ACCESSION	BI933998				
	VERSION	BI933998.1				
	KEYWORDS	EST.				
	SOURCE	tomato.				
	ORGANISM	Lycopersicon esculentum				
	REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.				
	AUTHORS	1 (bases 1 to 700) van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J., Uiterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.				
	TITLE	Generation of ESTs from tomato flower tissue, anthesis (2001)				
	JOURNAL	Unpublished (2001)				
	COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomics Institute Seq primer: T3.				
	FEATURES	Location/Qualifiers				
	source	1..700 /organism="Lycopersicon esculentum" /cultivar="T496" /db_xref="taxon:4081" /clone="cTOD18D11" /clone_id="tomato flower, anthesis" /lssue_type="flower" /dev_stage="anthesis" /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, T496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."				
	BASE COUNT	191 a 127 c 164 g 218 t				
	ORIGIN					
	Query Match	10.5%; Score 142; DB 10; Length 700;				
	Best Local Similarity	61.1%; Pred. No. 5.3e-22;				
	Matches 248; Conservative	0; Mismatches 155; Indels 3; Gaps 1;				
OY	195	tcagaagtcgctgttggagaggaatccaaagatctcggccggaatggaacctcgt	254			
Db	204	TCTGATGTAGTCGTGACCCGGCTTAGGATGTGCTTTGGGAGGAAGATGATTCATG	263			
OY	255	gataccaagaacgcgcgaacttaacttgatcgtcgtcgtcgtcagcgatggcgccctt	314			
Db	264	GATATGGCTCAGCGTCGCGGTGGTGTGTCATGCAATTTGCTGTGCTATTTGCACCC	323			
OY	315	tattcagctggagatcgcltttgatctctcttlaactctgttggttgcgaaggaggtc	374			
Db	324	ACTTTCAAATTAACCGCTGCTCTGGGATTCATTTGGTATATATGTAATC--ACTG	380			
OY	375	cttgatcacacttgctgttcacatagggctcttaactatcagtcgggtttcaagcttca	434			
Db	381	CTCGGTATTTAATCTTCTTTTCACGAAACCTCTCTCATAGAAAGTTCAAACTTCC	440			
OY	435	ttggttggaactctcttgctactgtygtctctcgtctcagtggaagatccatggaa	494			
Db	441	TGGCTTAATTAATCTTTTGGCTATGTGTGTGCAAGACCTTCAGGAGCATCATAT	500			
OY	495	ttggttggaacacataggtatccatccaccagttcgatcgatacgaagaagatgltcat	554			
Db	501	TGGGGACTTACTCATTAGGTACACCATATAGTTTGTGTGATTCAGAGAAAGACCC	560			

OY 555 ccacacaaagatttgcttcacatcggtggtttgaca 600
Db 561 CCTTATGAAAGATTGTGTCAGCATATGATGGGATGTTGATA 606

RESULT 14
BI931427
LOCUS
DEFINITION EST351316 tomato flower, 8 mm to preanthesis buds Lycopersicon
ACCESSION esculentum cDNA clone CTC20C17 5' end, mRNA sequence.
VERSION BI931427
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 721)
van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,
Ullterback,T., Van Aken,S., Romling,C.M., Nierman,W., Fraser,C.M.,
Martin,G.B., Giovannoni,J.J. and Tanksey,S.D.
Generation of ESTs from tomato flower tissue, buds 8 mm -
preanthesis
Unpublished (2001)
CONTACT: CUGI
JOURNAL Clemson University Genomics Institute
COMMENT 100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics
Institute
Seq primer: 73.
FEATURES
source Location/Qualifiers
1..721
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CTC20C17"
/clone_1lb="tomato flower, 8 mm to preanthesis buds"
/tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/note="Vector: pBluescript SK(-). Site_1: EcoRI. Site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
BASE COUNT 196 a 150 c 160 g 215 t
ORIGIN

Query Match 10.5%; Score 142; DB 10; Length 721;
Best Local Similarity 61.1%; Pred. No. 5.3e-22;
Matches 248; Conservative 0; Mismatches 155; Indels 3; Gaps 1;

OY 195 tcagaagtcgttcttgagagaatccaaagattctgcgcggaatgacacctcgt 254
Db 297 TCTGATGTCGTGCTGACCCGCTAGGAGATGCTTTGGGGAAGAAATGAAATCAATG 356
OY 255 gattatcaaaagccgctcaacttactgctcgtcgtcgtcgcgagatgcccctt 314
Db 357 GATATGGCTCAGCTGCGGTGGTGTGTATGATTTGCTGTGCTATTTGCACCCCTTT 416
OY 315 tatttcagctggagatcgcttcttgatctcttcttactctgcttggttcgaagcggtgt 374
Db 417 ACTTTCATATTAAGCTGCTCTTGGAATGATTTGGTATATGATATC---ACTGACTT 473
OY 375 ctgtgtatcacttctgcttccatagtggtcttactcactgagcggtttcaagcttcaag 434
Db 474 CTGGGATTTACACTTTCTTTTCACAGAAACCTCTCTCATAGAAATTTCAAACTTCCAAA 533

OY 435 ttgttgagactcttcttgctcacttgctctcgcctcttcagggagatccactgaga 494
Db 534 TGGCTGAATACCTTTTGGCTATTTGGTGTGCTCAAGCACTTACGAGCATTCATTTGAT 593
OY 495 tgggtgagcaaccatagatgacacacagcttcgtcgatcagaagaagatgtcactagt 554
Db 594 TGGGTGAGTACTCATATGATGTCACCACTATCACTTTTGATTCACAGAAAGACCTCACAG 653
OY 555 ccacacaaagatttgcttcacatcggtggtttgaca 600
Db 654 CCTTATGAAAGATTGTGTCAGCATATGATGGGATGTTGATA 699

RESULT 15
BI997512
LOCUS
DEFINITION 1031050C07.y2 C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BI997512
VERSION BI997512
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 660)
Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre
P., McDermott,J.P., Shrager,J., Sillflow,C. and Stern,D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Unpublished (2001)
CONTACT: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
source Location/Qualifiers
1..660
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3053"
/clone_1lb="C. reinhardtii CC-1690, Stress II (normalized)
, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Wells et al., (2000) Plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into Lambda
Zap II (Stratagene) in the EcoRI (5') and XhoI (3')
sites. pBluescript II SK- plasmids were excised from the
lambda ZAP clones by superinfection with Exsistist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
BASE COUNT 106 a 211 c 223 g 120 t
ORIGIN

Query Match 10.5%; Score 141.8; DB 10; Length 660;
Best Local Similarity 58.8%; Pred. No. 5.9e-22;
Matches 245; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

OY 638 caatggaatgattggaagaacagccttctacagatctccagaaacttatatgta 697

```
Db 41 CAACGGGACGACCTGGAGAGCAGTGGTACTACCGCTGGCTGGCGGACACTACCCCTT 100
QY 698 ccaatcaattggtcttaataagctcttaacttaactgaggggtttccatacatgtctg 757
Db 101 CCATGTGGCTGTGCTCAGCTGGCGGTGCTGTCTGTGGTGGTCCCGCGCTGTCTGTG 160
QY 758 gggaaatgggttttagatgtgtttatgttccattccacttcgctalcaactcagtttg 817
Db 161 GGGTGGCGCGCTGGCGCATGTGTCTGGGACATCATCGTGTGTAACCTGGGCTC 220
QY 818 tcataaatggggcggaagggcactggaatactggaattatcgaaaccaaatatgtttgt 877
Db 221 GCACTGTCTGGGGCTACCAAGGACTACACACCAGCGACCTGTGGAAGAACAACTGGTGGGT 280
QY 878 tgcattgtgtcgttttgagaggggtgtgcataaaccacacgcatcgaacaatcagc 937
Db 281 GGGCATTCCTGGGCTTTGGGAGGGGCTGGACACCAACCAACGCGCTTCGAGTTCTTGC 340
QY 938 tcgaacaggggtcgaatgtgtgcaagatcgatgttactgtgtacgtttalcaaggacltaca 997
Db 341 GCGCCACGGCTTCGAGTGTGTGGCAAGTGGACATGACCTGGTACATCATCTGGGCTCTCCA 400
QY 998 agctattgtgattgctaccaaatgtgaagctaaccaactgaagctcagaagcaaaaagct 1054
Db 401 GAAGGTGGGCTGGCCACCAAGTGAAGCTGCCACGGAGCGCCGAAGGCCAAAGCT 457
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Search completed: September 13, 2002, 08:11:11
Job time: 5536 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 08:45:51 ; Search time 61.47 Seconds

(without alignments)
643.278 Million cell updates/secTitle: us-09-664-840-2
Perfect score: 1946
Sequence: 1 LRSLYPPISISLSLEAM.....ATNKLPTAOKRIKAKSA 356Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_032802:*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1946	100.0	356	20	AAV39361
2	978.5	50.3	371	21	AAAG39561
3	969.5	49.8	371	21	AAAG21191
4	967.5	49.7	293	21	AAAG39562
5	958.5	49.3	293	21	AAAG21192
6	930	47.8	360	21	AAAG19661
7	930	47.8	361	21	AAAG19660
8	929	47.7	271	21	AAAG39563
9	920	47.3	307	21	AAAG21193
10	874.5	44.9	326	21	AAAG51215
11	874.5	44.9	326	21	AAAG51215

12	872	44.8	308	21	AAAG09499
13	872	44.8	327	21	AAAG09498
14	870.5	44.7	311	21	AAAG30599
15	788.5	40.5	300	21	AAAG21186
16	785.5	40.4	299	21	AAAG22905
17	785.5	40.4	313	21	AAAG22905
18	780.5	40.1	282	21	AAAG21187
19	771	39.6	309	21	AAAG09774
20	767.5	39.4	299	21	AAAG09774
21	689	35.4	272	16	AAAR76811
22	687	35.3	272	16	AAAR70260
23	650	33.4	318	16	AAAR70259
24	588.5	30.2	192	21	AAAG21188
25	556	28.6	278	16	AAAR76810
26	486.5	25.0	181	21	AAAG12679
27	484.5	24.9	160	21	AAAG12681
28	484.5	24.9	167	21	AAAG12680
29	367	18.9	128	21	AAAG16042
30	366.5	18.8	384	22	AAAB71665
31	359.5	18.5	461	22	AAAB64635
32	359	18.4	451	19	AAAW51087
33	354	18.2	445	19	AAAW70099
34	351.5	18.1	383	22	AAAB65786
35	351.5	18.1	383	22	AAAB66209
36	351.5	18.1	383	22	AAAB66210
37	351.5	18.1	383	22	AAAB71402
38	342.5	17.6	359	21	AAAG69378
39	342.5	17.6	359	22	AAAB44583
40	342	17.6	354	13	AAAR25853
41	336.5	17.3	359	21	AAAG69377
42	335	17.2	330	22	AAAG63850
43	335	17.2	330	22	AAAG63934
44	335	17.2	330	22	AAAG63225
45	329.5	16.9	358	22	AAAB44582

ALIGNMENTS

RESULT 1	
AAV39361	
ID	AAV39361 standard; Protein: 356 AA.
XX	
AC	AAV39361;
XX	
DT	20-DEC-1999 (first entry)
XX	
DE	Delta-5 acyl-CoA desaturase.
XX	
KW	Delta-5 acyl-CoA desaturase; double bond; plant membrane; neutral lipid;
KW	seed tissue; palmitoyl-CoA; oleoyl-CoA; fatty acid elongase; biopolymer;
KW	biosynthetic pathway; lubricant; grease; plastic; ink; cosmetic;
KW	surfactant; biodegrade; long shelf life.
XX	
OS	Limnathes douglassi.
XX	
PN	W09949050-A2.
XX	
PD	30-SEP-1999.
XX	
PF	12-MAR-1999; 99MO-US05471.
XX	
PR	20-MAR-1998; 98US-0078736.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E. I.
XX	
PI	Cahoon EB, Hiltz WD, Kinney AJ, Vollmer SJ;
XX	
DR	WPI: 1999-591101/50.
XX	
DR	N-PDB; AA28315.
XX	
PT	Nucleic acid fragments useful in the production of industrial agents
PT	for eg. lubricants or cosmetics -

XX Claim 1; Page 46-47; 54pp; English.
 PS This is the amino acid sequence of the Limnanthes douglasii delta-5
 CC acyl-CoA desaturase. Delta-5 desaturase introduces a double bond at the
 CC delta 5 position of a C20 fatty acid. Delta-5 desaturase is an enzyme
 CC which is able to further desaturate mono-unsaturated fatty acids to make
 CC poly-unsaturated fatty acids. Fatty acids are used in plant membranes
 CC and in neutral lipids that are formed for the storage of energy in
 CC developing seed tissue. The delta-5 desaturase nucleotide sequence can be
 CC linked to regulatory sequences and used to transform host cells. The
 CC invention also reveals a fatty acyl-CoA elongase amino acid sequence
 CC (AAV39362), this enzyme prefers palmitoyl-CoA (16:0-CoA) as its substrate
 CC instead of oleoyl-CoA (18:1-CoA) the usual substrate for the known plant
 CC fatty acid elongase. The nucleic acid sequences of the delta-5 desaturase
 CC and the acyl-CoA elongase can be used in genetic engineering to
 CC manipulate fatty acid biosynthetic pathways, allowing changes to be made
 CC in the fatty acid composition of plants and or oils and to introduce new
 CC pathways in to oil seeds in order to produce new biopolymers from
 CC acyl-CoA. The oils and fatty acids produced by the genetically engineered
 CC plants have potential for use as industrial agents including lubricants,
 CC greases, plastics, inks, cosmetics and surfactants. Polyestolides derived
 CC from the 20:1 delta-5 fatty acids of Limnanthes biodegrade slower than
 CC those derived from soybean oils or oleic oils, and thus will produce
 CC industrial products with a longer shelf life.
 CC
 XX Sequence 356 AA;

Query Match 100.0%; Score 1946; DB 20; Length 356;
 Best Local Similarity 100.0%; Pred. No. 2.1e-197;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRLSLYPTISISLSLRLAMASFIATTPAMPAPASVLDPKIPKPEKTEPRKPDLE 60
 Db 1 LRLSLYPTISISLSLRLAMASFIATTPAMPAPASVLDPKIPKPEKTEPRKPDLE 60
 QY 61 RFRISVVLEKRSKGFWRKRNPRDIONAVTLVLHALLAAMAFYSWDAWISFILLGF 120
 Db 61 RFRISVVLEKRSKGFWRKRNPRDIONAVTLVLHALLAAMAFYSWDAWISFILLGF 120
 QY 121 ASGVGILCLCFRCLTHGSGFLKPLVEYEFACGSLALOGDPMENVRNRYHNOVDPR 180
 Db 121 ASGVGILCLCFRCLTHGSGFLKPLVEYEFACGSLALOGDPMENVRNRYHNOVDPR 180
 QY 181 DVHSPFQGFWECHIGWVLDKDLFEKRGGRNNVNDLKKQAFYRFLQKTYMHQALATL 240
 Db 181 DVHSPFQGFWECHIGWVLDKDLFEKRGGRNNVNDLKKQAFYRFLQKTYMHQALATL 240
 QY 241 LYYVGFYIYWGKGFRLVPEHSTFAINSVCHKKGSRPNTGDI STNNMFALCAFGEG 300
 Db 241 LYYVGFYIYWGKGFRLVPEHSTFAINSVCHKKGSRPNTGDI STNNMFALCAFGEG 300
 QY 301 WHNNHAFEOSARHGLEMMWQIDVTWYVIRTLQALIGLATNVKLPTEAOKOKLAKKSA 356
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RESULT 2
 AAG39561 ID AAG39561 standard; Protein: 371 AA.
 AC AAG39561;
 DT 18-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 48968.
 DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS

XX EP1033405-A2.
 PN 06-SEP-2000.
 PD 25-FEB-2000; 2000EP-0301439.
 XX 25-FEB-1999; 99US-0121825.
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Query Match 50.3%; Score 978.5; DB 21; Length 371;
Best Local Similarity 56.2%; Pred. No. 6,7e-95;
Matches 173; Conservative 52; Mismatches 80; Indels 3; Gaps 3;

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DB 121 fgfnwraaveafgly-ivglllgltlsfhnshkafklpkwleylfaycgaqalqgnrl 179
QY 164 EWSNHRVYHQQVTERDVHSPTQGFWFCIHGVNLKDLFEVKEGGRNNVNDLKRQAFV 223
DB 180 dwtsthrlyhgfcdsdrpdrpsldgfwfshmmwfdntc-ltqrcgepnnvglckpfy 238
QY 224 RFLQKTYMHNOLALLLVYVGFRPYIVWGMGRLYPMRSTRAINSVCHKMGGRPMNG 283
DB 239 flrttlyllhplalavalyamgfigpflvwgmgyrtlwvyltlvlnsacvkgqwnr 298
QY 284 DISTNNNFVALCFGEGMNNHHAFQSAHGLEMMQIDVTWVIRTLQIGLATVWKLP 343
DB 299 dlsknmwvaalafgegwinnhhafefsarhglewqldmtwvvlfgalglatclvklp 358
QY 344 TEAQOKL 351
DB 359 seaqkgqm 366

RESULT 3
AAG21191

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DE	Arabidopsis thaliana protein fragment SEQ ID NO: 23657.	
XX	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX	Arabidopsis thaliana.	
OS	Arabidopsis thaliana.	
XX	EP1033405-A2.	
PN	06-SEP-2000.	
XX	25-FEB-2000; 2000EP-0301439.	
PF	25-FEB-1999; 99US-0121825.	
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AC AAC21192;
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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DB	62 llytllstfltrnshkafkrlpkwleylfaycgagailqgnridvstshryhbfcdsdrph	121		
OY	164 SFTGCFWCHIGVLDKDLFEKRCGRKNNVNDLKKAFYFLOKTYTHQALALIALLY	243		
DB	122 spldglfwishnmwldnt-ltqrcgepnvgylekqpfyflfcttlyllhplalavalay	180		
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OY	304 NHAEQASRHGLEWMOIDVTWYTRTLQATGLATNVLPTPEAKOKL	351		
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XX	hybridisation assay; genetic mapping; gene expression control; promoter;			
XX	termination sequence.			
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
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PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159329.
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PR 22-OCT-1999; 99US-0160989.
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PR 29-OCT-1999; 99US-0162142.

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Query Match 47.8%; Score 930; DB 21; Length 361;
Best Local Similarity 55.1%; Pred. No. 8.8e-90;
Matches 168; Conservative 39; Mismatches 92; Indels 6; Gaps 4;

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QY 51 ETPEKPDDEFRPTSEVYLERKSKGFWRKRNPRDIONAVTLVLNALAAMPFYFSWDA 110
DB 61 eapdhvesswrrllsevvvrtktrsfwerstswdsklvlfygtllsllepffyswda 120
QY 111 FWISFILLGSPAGVLTITLCFHRCLTFHGFKLPKLVYFPAYGSLALOGDPHEWNSNR 170
DB 121 fw-fpwlvfinglc-llsyhnlslrstdlpwleylta99vtafgdplewshnr 178
QY 171 YHQPVDTERDVHSPQGFNFCHIGWVLDKDLFEVKRGRNRNVNDLKOAFYFLQKTY 230
DB 179 ynhkhetqtrpspcgfwfshnawifdtsllenogv-eeavddlvrgpfyrlqtrv 237
QY 231 MYHQLALIALLYVGGPRYVWGMGRFLVFMFSTRAINSVCKRWGGRPNWTDLSNNM 290
DB 238 llmmaystlfytcgmpillwgitlavrlhlftfvsvchlwtrawtsdfsknw 297
QY 291 FVALCAFGEGMNNHHAFEGSARHGLEMMQIDVTWVYIRFLAIGLATNVKLPTEAKOK 350
DB 298 wvalcltgcgwhnnhahfetsarhglewgdltwcllrlfaiglatnvklpcteq--- 354
QY 351 LKAAS 355
DB 355 mkgka 359

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RESULT 8
ID AAG39563 standard; Protein; 271 AA.
XX
AC AAG39563;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48970.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX

PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-0301439.	
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PR	30-JUN-1999; 99US-0141287.	
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PR	26-AUG-1999; 99US-0150884.	
PR	27-AUG-1999; 99US-0151065.	
PR	27-AUG-1999; 99US-0151066.	
PR	27-AUG-1999; 99US-0151080.	
PR	30-AUG-1999; 99US-0151303.	
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PR	01-SEP-1999; 99US-0151930.	
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PR	10-SEP-1999; 99US-0153070.	
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PR 29-SEP-1999; 99US-0156596.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 47.7%; Score 929; DB 21; Length 271;
Best Local Similarity 60.7%; Pred. No. 7, 6e-90;

Matches 162; Conservative 43; Mismatches 60; Indels 2; Gaps 2;

OY 85 DIGNATLLVLAHLMAMAPRYEFSMDAFWISFILLGFASSVGLGTLTCHRLTNGGRLLPK 144
DB 2 dfgavavvsmhlslslrlqfmlravsvafgly-lvtgllgtlflshfnlshkafk1pk 60
OY 145 LVEYFFAYCGSLALQGDPRMEVSNHRYHOFVTERDVHSPRTQGFMCNIGWLDKDLFV 204
DB 61 wleyllfaycgagqlggnrlqfmlravsvafgly-lvtgllgtlflshfnlshkafk1pk 119
OY 205 EKRGRNNVNDLKKQAFYRFLQKTYMYHQLALALLLVYVGFRPYIWMGMPRLVFMFHS 264
DB 120 tfgcgepnvvgdlkqpfyflfctyllhplalavalymgfrflvmgmvrlvwyhl 179
OY 265 TFAINVCVCHKMGSRFWMTGSLSTNNMFVALCAGEGCHNNHNAFEOSARGLGEMWQIDVT 344
DB 180 twnlvnascchwqgawltglsknwvaalafggwghnnhhafehsahglawqldmt 239
OY 325 WYVIRTLQALIGLATNFKLPTEAKOKL 351
DB 240 wyyvkkflqalglatdtklpsaaqkqcm 266

RESULT 9

AMG21193
ID AMG21193 standard; Protein; 271 AA.

XX
AC AMG21193;

XX
DT 17-OCT-2000 (first entry)

XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23659.

XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.

RESULT 10
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ID AAG51216 standard; Protein: 307 AA.
XX AAG51216;
XX
XX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64979.
KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX EPI033405-A2.
XX
XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 99US-0126785.
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PR 23-APR-1999; 99US-0130510.
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AA051215;

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 64978.

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

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Best Local Similarity 52.28; Pred. No. 1,1e-83;
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OY 181 DVHSPGCFMFCIHGWLDKDLFEKRGGRNNVNDLKKAFYRFLQRTYMHQALIAL 240
DB dphapkegfwfshllwlydsaylvsk-cgrtanvedlkrqfkyfllqkvtvlfhllgltff 212
OY 241 LYYGCGPRTYIWMGFRLEVFEMHSTFALINSVCHKMGGRPNNTGDLSTNNFVALCARFEG 300
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RESULT 14

AAG30599
ID AAG30599 standard; protein; 311 AA.

XX AAG30599;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 36610.

KW Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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Oy 122 SGVLGTLTCEHRCILTHGGCFKLKLEYEFYFAYGSLALOGDPMEMVSNHRRHNHOFVDERD 101
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Oy 299 EGHNNHNAFEBOSARHGLEMMQIDTWVYVIRLQALIGATVWKLPTPEBOKOL 351
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DT 17-OCT-2000 (first entry)

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KW protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

06-SEP-2000. PD

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

09-MAR-1999; 99US-0123548.

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PR 06-APR-1999; 99US-0128234.
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.
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PR 19-JUL-1999; 99US-0144334.
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PR 12-AUG-1999; 99US-0148341.
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PR 16-AUG-1999; 99US-0149368.
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PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149902.
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PR 25-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 29-SEP-1999; 99US-0156596.
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PR 07-OCT-1999; 99US-0158029.
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PR 12-OCT-1999; 99US-0158369.

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PR 13-OCT-1999; 99US-0159293.  
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PR 21-OCT-1999; 99US-0160770.  
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PR 22-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.
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Query Match 40.5%; Score 788.5; DB 21; Length 300;
Best Local Similarity 50.2%; Pred. No. 6.6e-75;

Matches 144; Conservative 46; Mismatches 94; Indels 3; Gaps 2;

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DB 13 srvtatmqktrayfgxqwpdvdrasvvivhflclapfnfkwa--lrfglvlfalt 70  
OY 125 LGITLCFHRCLTHGCFKLPKLVYEFPAFCGSLALOGDPMEWVSNHRYHQVYTERDVHS 184  
DB 71 lsitfsftrnlshtsrsklpkwlcpwysavfalqgdpmdwslhrfthqfidsdrphs 130  
OY 185 PTOGFWPGHIGVLDKDLFEVERKGRNNVNDLKKOAFYRFLOKTYMTHQALALALVYV 244  
DB 131 pkeglilfshilwifdtykykcggrdnvidlkkqwfylitrliaavhlmfwtclily 189  
OY 245 GGFPIYVGMGFRVLMFMEHSTFAINSVCHKMGGRPMNTGDLSTNNMFVALCAFGEGWHNN 304  
DB 190 gglpyrltcggvgfyfigyhvtwlvnsachlwsrwnlckdsrvnwawlsifmgeswhnn 249  
OY 305 HHAPEQSARHGLEMMQIDVTWVIRTLQALIGLATNVKLPTEAKOKL 351  
DB 250 hhafeasarqglewqidlwtlylrlfavlglatvklipseidqkqm 296
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Search completed: September 13, 2002, 09:48:35
Job time: 3764 sec

GenCore version 4.5
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OM proteIn - protein search, using sw model

Run on: September 13, 2002, 08:47:00 ; Search time 24.84 seconds
(without alignments)
350.061 Million cell updates/sec

Title: US-09-664-840-2
Perfect score: 1946
Sequence: 1 LRSLYFPISLISLSLEAM.....ATNWKLPTEAKOKLAKSA 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	650	33.4	318 1	US-08-309-182B-3 Sequence 3, Appl
2	555	28.6	278 3	US-08-663-082-4 Sequence 4, Appl
3	349.5	18.0	358 2	US-08-558-823-19 Sequence 19, Appl
4	326	16.8	510 1	US-08-742-273-2 Sequence 2, Appl
5	323.5	16.6	349 2	US-08-558-823-4 Sequence 4, Appl
6	273.5	14.1	182 2	US-08-558-823-5 Sequence 5, Appl
7	178	9.1	65 3	US-08-663-082-2 Sequence 2, Appl
8	111.5	5.7	378 2	US-08-244-205-7 Sequence 7, Appl
9	111.5	5.7	378 2	PCT-US92-10284-7 Sequence 7, Appl
10	111.5	5.7	404 2	US-08-244-205-9 Sequence 9, Appl
11	111.5	5.7	404 2	PCT-US92-10284-9 Sequence 9, Appl
12	108.5	5.6	446 2	US-08-244-205-5 Sequence 5, Appl
13	108.5	5.6	446 4	US-09-161-994A-6 Sequence 6, Appl
14	108.5	5.6	446 4	US-09-161-994A-7 Sequence 7, Appl
15	108.5	5.6	446 5	PCT-US92-10284-5 Sequence 5, Appl
16	104.5	5.4	446 5	PCT-US94-01321-10 Sequence 10, Appl
17	101.5	5.4	402 4	US-09-025-578-2 Sequence 2, Appl
18	101.5	5.2	329 4	US-09-161-994A-6 Sequence 6, Appl
19	99	5.1	446 4	US-09-161-994A-7 Sequence 7, Appl
20	98.5	5.1	447 4	US-09-161-994A-8 Sequence 8, Appl
21	95.5	4.9	435 5	PCT-US94-01321-12 Sequence 12, Appl
22	94.5	4.9	460 3	US-08-689-974-5 Sequence 5, Appl
23	94.5	4.8	460 3	US-09-058-376-5 Sequence 5, Appl
24	94	4.8	383 3	PCT-US94-01321-2 Sequence 2, Appl
25	92.5	4.8	1865 1	US-08-588-985-2 Sequence 2, Appl
26	92.5	4.8	1865 1	US-08-971-988-2 Sequence 2, Appl
27	90	4.6	377 4	US-09-161-994A-12 Sequence 12, Appl

28	90	4.6	453 2	US-08-244-205-13 Sequence 13, Appl
29	90	4.6	453 4	US-09-161-994A-10 Sequence 10, Appl
30	90	4.6	453 5	PCT-US92-10284-13 Sequence 13, Appl
31	85	4.4	365 2	US-08-833-610-7 Sequence 7, Appl
32	85	4.4	365 3	US-08-834-033A-17 Sequence 17, Appl
33	84	4.3	213 4	US-09-107-383-14 Sequence 14, Appl
34	84	4.3	386 2	US-08-244-205-2 Sequence 2, Appl
35	84	4.3	386 4	US-09-161-994A-11 Sequence 11, Appl
36	84	4.3	386 5	PCT-US92-10284-2 Sequence 2, Appl
37	82.5	4.2	1455 3	US-08-840-062-5 Sequence 5, Appl
38	81	4.2	316 4	US-08-961-083-156 Sequence 156, App
39	79	4.1	641 4	US-08-961-083-160 Sequence 160, App
40	78.5	4.0	383 4	US-09-059-769-12 Sequence 12, Appl
41	78.5	4.0	383 4	US-09-161-994A-16 Sequence 16, Appl
42	78.5	4.0	461 2	US-08-672-814D-2 Sequence 2, Appl
43	78.5	4.0	461 2	US-09-333-696-2 Sequence 2, Appl
44	78	4.0	1311 2	US-08-540-406-4 Sequence 4, Appl
45	78	4.0	1311 3	US-08-656-055-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-309-182B-3
; Sequence 3, Application US/08309182B
; Patent No. 5639645
GENERAL INFORMATION:
; APPLICANT: NO. 563964510 MURATA
; TITLE OF INVENTION: A RECOMBINANT 9 DESATURASE AND A GENE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; STREET: Wenderoth, Lind & Ponack
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/309, 182B
; FILING DATE: September 20, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-309-182B-3

Query Match 33.4%; Score 650; DB 1; Length 318;
Best Local Similarity 45.5%; Pred. No. 3.7e-64;
Matches 116; Conservative 48; Mismatches 87; Indels 4; Gaps 2;

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;          TOPOLOGY: linear
;          ORIGINAL SOURCE:
;          ORGANISM: Ancyclostis nidulans
;          STRAIN: R2-Spc
;          US-08-663-082-4

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		Mismatches	146;
		Indels	45;
		Gap	0;

	Best local similarity	29.5%	Pred. No. 9.1e-28:		
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QY	157	ALQGDMEVSNHRYHNO	VDFTERDSQPFMCHIGVWLDKDLFYKRCGRNRNVND	216	
Db	186	SVESGAKKMGHSHRIHNR	ITDTLRDRYDARRGLMSTHMGWMLLKP	---NPKYKARADITD 242	
QY	217	LKKQAFRFLQATYMHQI	-----ALIALLY	---YVGGFPRIYMGGMFRLVEMF	-HST 265
Db	243	MDDMTIRPHNHLYLML	TLTAFTVPIITLCIGFYFNDYMGCLY	---AGFIVFVIGQAT 298	
QY	266	FAINSVCYHMGGRPNMT	GDLSITNNMFVNLCAFGEGMHNHNAF	EDSARIRGLEMTQIDYTW 325	
Db	299	FCINSLAHYICQRPDD	RTRTPRDNMTITLVYFGEQYHNHNEEPDYRNALMKWYDPTK 358		
QY	326	YVIRFLQALGLATNVK	-----LPTAQOK	---KLIAK 354	
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 Db 85 ARLMTHTKFAKLPLEIYLMIFNSLAFONTAITWAREHRLHHKSDTDADPHNARSQPF 144
 QY 191 FCHIGVNDKDLFEVKKRGRNNVNDLKKQAFYRFLOKTYMHOL-----ALIALLYVVG 245
 Db 145 YSHVGMVLVKKHPDVKYGTIDMSDVNNPYLKF-QKKYAVPLIGYCFALPTLI----- 199
 QY 246 GPPYIWMG-----FRLVFMFHSSTFAINSYCHKRGGRPNWTGDLSTNNFVALCA 296
 Db 200 --PYCWMGSMNNAMHIALFRITFPLNTVFLVNSAHHWGNKPYDKSLIPQNLVSELA 257
 QY 297 FEGGWHNNHAF 308
 Db 258 SGEGFHNHAF 269

RESULT 6

US-08-558-823-5
 ; Sequence 5, Application US/08558823
 ; Patent No. 5876994
 ; GENERAL INFORMATION:
 ; APPLICANT: Knipple, Douglas C.
 ; APPLICANT: Roelofs, Wendell L.
 ; APPLICANT: Miller, Stuart J.
 ; TITLE OF INVENTION: PHEROMONE DESATURASES
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 ; STREET: Clinton Square, P.O. Box 1051
 ; CITY: Rochester
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 14603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/558,823
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rogalsky Esq., Peter
 ; REGISTRATION NUMBER: 38,601
 ; REFERENCE/DOCKET NUMBER: 19603/400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (716) 263-1634
 ; TELEFAX: (716) 263-1600
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 182 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-558-823-5

Query Match 14.1%; Score 273.5; DB 2; Length 182;
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 Matches 60; Conservative 31; Mismatches 77; Indels 21; Gaps 4;

QY 132 HRCITHGCGFLPKLVEFFAYCGSLAQGDPMWVSNRRYHGFVTERDVHSTPGFW 191
 Db 1 HRMSHTKFAKLPLEIYLMIFNSLAFONTAITWAREHRLHHKSDTDADPHNARSQPF 60
 QY 192 CHIGVNDKDLFEVKKRGRNNVNDLKKQAFYRFLOKTYMHOL-----ALIALLYVVG 246
 Db 61 SHVGMVLVKKHPDVKYGTIDMSDVNNPYLKF-QKKYAVPLIGYCFALPTLI----- 114

QY 247 FRYIWMG-----FRLVFMFHSSTFAINSYCHKRGGRPNWTGDLSTNNFVALCA 297
 Db 115 -PYCWMGSMNNAMHIALFRITFPLNTVFLVNSAHHWGNKPYDKSLIPQNLVSELA 173
 QY 298 GEGWHNNH 306
 Db 174 GEGFHNH 182

RESULT 7

US-08-663-082-2
 ; Sequence 2, Application US/08663082
 ; Patent No. 6043411
 ; GENERAL INFORMATION:
 ; APPLICANT: NISHIZAWA, Osamu
 ; APPLICANT: TOGURI, Toshihiro
 ; TITLE OF INVENTION: GENE FOR FATTY ACID DESATURASE, VECTOR
 ; TITLE OF INVENTION: CONTAINING SAID GENE, PLANT TRANSFORMED WITH SAID GENE,
 ; AND PROCESS FOR CREATING SAID PLANT
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/663,082
 ; FILING DATE: 25-JUN-1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/JP94/02288
 ; FILING DATE: 28-DEC-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 93/352858
 ; FILING DATE: 28-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 81356/107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 65 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; ORIGINAL SOURCE:
 ; ORGANISM: Anabaena variabilis
 ; STRAIN: IAM M-3
 ; US-08-663-082-2

Query Match 9.1%; Score 178; DB 3; Length 65;
 Best Local Similarity 49.2%; Pred. No. 1.5e-12;
 Matches 32; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 236 ALIALLYYGGPPYIWMGFFRLVFMFHSSTFAINSYCHKRGGRPNWTGDLSTNNFVALC 295
 Db 1 ALGLLLIYLGWGSFYVWGVFFRLVWYHCTWLVNSATHTKFGRTYDADGRSTNCWMAVL 60
 QY 296 AFEGG 300
 Db 111

QY 193 -----HIGWVL-----DKDLFEVKKGRGRNNVNDLKKQAFYFLQKTYMY 232
 Db 195 LPLVMLATPYPLMARSPPGKSGHYHPDSDLPRK-----ERNVDY-----LSTACW 240
 QY 233 HOLA-LIALLYVVG-----FPY-----IWMGGRFLVFMFHSFPAINSVCHK----- 274
 Db 241 TMAVAVLLVCLNFMGMQMLKLYIPYINVM-LDF-VTYLHHHG-----HEDKLPW 291
 QY 275 MGRPN--TGDLST-----NMFEVALCAFGEGMNNHNAFEQSARHGL 316
 Db 292 YMGKESYLRGGLTTLDRDYGILNNIHDI-----GTHVHHLFPQIPHYHL 338

RESULT 12

US-08-244-205-5
 ; Sequence 5, Application US/08244205
 ; Patent No. 5952544
 ; GENERAL INFORMATION:
 ; APPLICANT: Browae, John, Kinney, Anthony J.,
 ; APPLICANT: Pierce, John, Wierzbicki, Anna M.,
 ; APPLICANT: Yadev, Narendra S., Perez-Grau, Luis
 ; TITLE OF INVENTION: Fatty Acid Desaturase Genes
 ; TITLE OF INVENTION: from Plants
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: E. I. du Pont de Nemours and Company
 ; STREET: 1007 Market Street
 ; CITY: Wilmington
 ; STATE: Delaware
 ; COUNTRY: U.S.A.
 ; ZIP: 19898
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: Macintosh System, 6.0
 ; SOFTWARE: Microsoft Word, 4.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/244, 205
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/804, 259
 ; FILING DATE: 4 DECEMBER 1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Floyd, Linda A.
 ; REGISTRATION NUMBER: 33,692
 ; REFERENCE/DOCKET NUMBER: BB-1036-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (302) 992-4929
 ; TELEFAX: (302) 892-7949
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 446 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-244-205-5

Query Match 5.6%; Score 108.5; DB 2; Length 446;
 Best Local Similarity 22.0%; Pred. No. 0.0013;
 Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;
 QY 1 LRLSLYFPISSISLSLEAMASF-----IATTP-AMPAFASVLDPKIPTRPEPKTTPK 54
 Db 36 LSSSSYKTSSTSSPLSGFNSRDGFTRNWALNVSTPLTPIF-----EESPL 80
 QY 55 PKDLEFRFTSEV-----VLERKSGFW-RRKWP-----RDIONAVTLVLHALLAM 101
 Db 81 EEDNKGRRFPGAPPPFNADIIRAIKHCWKNPKWSLSYVADV-----AIVFALAAG 134
 QY 102 APF-----YESWDAFWISFILLGFASGVIGITLCFHRCLTHGFG-----KLPKLYVEFFAYCG 154

Db 135 AAYLNNTIWPDLTWLAOGTFEMALFVLG-----HDC-GHGSFSDNDRKLSVGHLLHSSI 188
 QY 155 SLALQDPMEMVSNHRYNHQ-----FVDERDVH-----SPNOGFWFC----- 192
 Db 189 LVPYHG-----WRISHRTHQNHGHVENDSEWHMSEKIYTLTKPRFRFTPLPLVMLAY 244
 QY 193 -HIGWVL-----DKDLFEVKKGRGRNNVNDLKKQAFYFLQKTYMYHOLA--LI 238
 Db 245 PFLYLMARSPPGKSGHYHPDSDLPRK-----ERKDV-----LSTACWTAMALLAY 290
 QY 239 ALLYYVG-----GPPY-----IWMGGRFLVFMFHSFPAINSVCHK-----WGRPN- 281
 Db 291 CLNFTTGPIMKMLXGIPYINVM-LDF-VTYLHHHG-----HEDKLPWYRGKESY 341
 QY 282 -TGDLST-----NMFEVALCAFGEGMNNHNAFEQSARHGL 316
 Db 342 LRGLTTLDRDYGILNNIHDI-----GTHVHHLFPQIPHYHL 380

RESULT 13

US-09-161-994A-5
 ; Sequence 5, Application US/09161994A
 ; Patent No. 6333448
 ; GENERAL INFORMATION:
 ; APPLICANT: BAFOR, Maureen
 ; APPLICANT: BANAS, Antoni
 ; APPLICANT: DAHLQVIST, Anders
 ; APPLICANT: CUMMIESON, Per-Olov
 ; APPLICANT: LEE, Michael
 ; APPLICANT: SJODAL, Staffan
 ; APPLICANT: STYVNE, Sten
 ; APPLICANT: LENMAN, Marit
 ; TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
 ; FILE REFERENCE: BAFOR-1
 ; CURRENT APPLICATION NUMBER: US/09/161, 994A
 ; PRIOR FILING DATE: 1998-09-29
 ; PRIOR APPLICATION NUMBER: 9601236.4
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 446
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-161-994A-5

Query Match 5.6%; Score 108.5; DB 4; Length 446;
 Best Local Similarity 22.0%; Pred. No. 0.0013;
 Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;
 QY 1 LRLSLYFPISSISLSLEAMASF-----IATTP-AMPAFASVLDPKIPTRPEPKTTPK 54
 Db 36 LSSSSYKTSSTSSPLSGFNSRDGFTRNWALNVSTPLTPIF-----EESPL 80
 QY 55 PKDLEFRFTSEV-----VLERKSGFW-RRKWP-----RDIONAVTLVLHALLAM 101
 Db 81 EEDNKGRRFPGAPPPFNADIIRAIKHCWKNPKWSLSYVADV-----AIVFALAAG 134
 QY 102 APF-----YESWDAFWISFILLGFASGVIGITLCFHRCLTHGFG-----KLPKLYVEFFAYCG 154
 Db 135 AAYLNNTIWPDLTWLAOGTFEMALFVLG-----HDC-GHGSFSDNDRKLSVGHLLHSSI 188
 QY 155 SLALQDPMEMVSNHRYNHQ-----FVDERDVH-----SPNOGFWFC----- 192
 Db 189 LVPYHG-----WRISHRTHQNHGHVENDSEWHMSEKIYTLTKPRFRFTPLPLVMLAY 244
 QY 193 -HIGWVL-----DKDLFEVKKGRGRNNVNDLKKQAFYFLQKTYMYHOLA--LI 238
 Db 245 PFLYLMARSPPGKSGHYHPDSDLPRK-----ERKDV-----LSTACWTAMALLAY 290
 QY 239 ALLYYVG-----GPPY-----IWMGGRFLVFMFHSFPAINSVCHK-----WGRPN- 281

Db 291 CLNFTTGPLOMLKLYGIPYINWMM-LDF-VTYLHHHG-----HBDKLPWYRGKEMSY 341

QY 282 -TGDLST-----NNMFVALCAGGEGWNNHNAFEQASRHGL 316

Db 342 LRGLTTLDRDYGILNNIHDI-----GTHVHHLFPOLPHYHL 380

RESULT 14
PCT-US92-10284-5
Sequence 5, Application PC/TUS9210284

GENERAL INFORMATION:
APPLICANT: Browne, John, Kinney, Anthony J.,
APPLICANT: Pierce, John, Wierzbicki, Anna M.,
APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
TITLE OF INVENTION: Fatty Acid Desaturase Genes
TITLE OF INVENTION: Itom Plants
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10284
FILING DATE: 19921203
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/804,259
FILING DATE: 4 DECEMBER 1991
ATTORNEY/AGENT INFORMATION:
NAME: Floyd, Linda A.
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1036-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-10284-5

Query Match 5.6%; Score 108.5; DB 5; Length 446;
Best Local Similarity 22.0%; Pred. No. 0.0013;
Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;

QY 1 LRLSLYFPISLSLSLEAMASF-----IATTP-AMPAFASVLDPKIPKPEKTEPK 54
Db 36 LSSSYKTSSPLSFGINSRSGFTRNNALNVSTPLTPIF-----EESPL 80
QY 55 PKDLERFRTSEV-----VLERKSKGFV-RRKNP-----RDIONAVTLVLHAIAM 101
Db 81 EEDNQRDPGAPPPFNADIRAIIPKHCWKPKMSLSYVVRDY-----AIFALAAAG 134
QY 102 APF---YFSWDAFWISFTILGFASGVLTICFHRCLTHGCF---KLPKLVEFFAYCG 154
Db 135 AAYLNMMIYWPPLYWLAOGTFMALFVLG---HDC-GHGSFSDPKLNSVYGHLLHSSI 188
QY 155 SLALOGDPMEWVSNRHYHQ---FVDTERDVH-----SPTQGFWFC-----192
Db 189 LVPYHG---WRISHRTHQNHGHVENDSWHPSEKITYNTLDKPTREFRFTLPLVMLAY 244

QY 193 -HIGWVL-----DKDLFEVKRGRNNVNDLKKQAFYRFLQKTYMHOLA--LI 238
Db 245 PFYLMARSPGKSGSHYHPDSLFLPK---ERKDY-----LSTACTATMAALLV 290
QY 239 ALLXYVG-----GFPY---IWMGMGRFLVEMFSTFPAINSVCHK---WGGRPNV- 281
Db 291 CLNFTTGPLOMLKLYGIPYINWMM-LDF-VTYLHHHG-----HBDKLPWYRGKEMSY 341

QY 282 -TGDLST-----NNMFVALCAGGEGWNNHNAFEQASRHGL 316

Db 342 LRGLTTLDRDYGILNNIHDI-----GTHVHHLFPOLPHYHL 380

RESULT 15
PCT-US94-01321-10
Sequence 10, Application PC/TUS9401321

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Altered linoleic and linoleic Acid Content
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 72
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01321
FILING DATE: 04-FEB-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156551
FILING DATE: 22-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014431
FILING DATE: 05-FEB-1993
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-01321-10

Query Match 5.6%; Score 108.5; DB 5; Length 446;
Best Local Similarity 22.0%; Pred. No. 0.0013;
Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;

QY 1 LRLSLYFPISLSLSLEAMASF-----IATTP-AMPAFASVLDPKIPKPEKTEPK 54
Db 36 LSSSYKTSSPLSFGINSRSGFTRNNALNVSTPLTPIF-----EESPL 80
QY 55 PKDLERFRTSEV-----VLERKSKGFV-RRKNP-----RDIONAVTLVLHAIAM 101
Db 81 EEDNQRDPGAPPPFNADIRAIIPKHCWKPKMSLSYVVRDY-----AIFALAAAG 134
QY 102 APF---YFSWDAFWISFTILGFASGVLTICFHRCLTHGCF---KLPKLVEFFAYCG 154
Db 135 AAYLNMMIYWPPLYWLAOGTFMALFVLG---HDC-GHGSFSDPKLNSVYGHLLHSSI 188
QY 155 SLALOGDPMEWVSNRHYHQ---FVDTERDVH-----SPTQGFWFC-----192
Db 189 LVPYHG---WRISHRTHQNHGHVENDSWHPSEKITYNTLDKPTREFRFTLPLVMLAY 244
QY 193 -HIGWVL-----DKDLFEVKRGRNNVNDLKKQAFYRFLQKTYMHOLA--LI 238
Db 245 PFYLMARSPGKSGSHYHPDSLFLPK---ERKDY-----LSTACTATMAALLV 290
QY 239 ALLXYVG-----GFPY---IWMGMGRFLVEMFSTFPAINSVCHK---WGGRPNV- 281
Db 291 CLNFTTGPLOMLKLYGIPYINWMM-LDF-VTYLHHHG-----HBDKLPWYRGKEMSY 341

Fri Sep 13 15:31:16 2002

us-09-664-840-2.rai

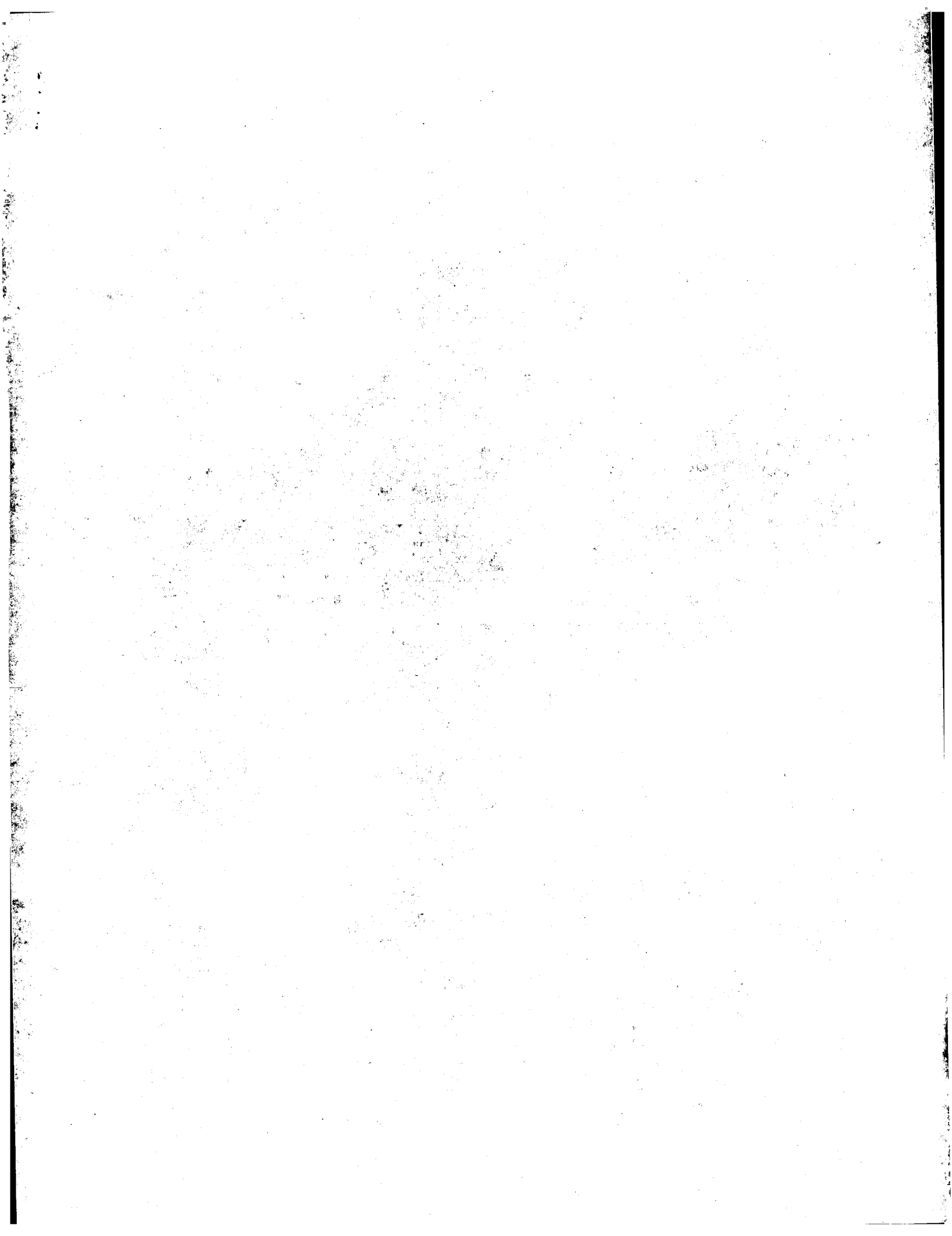
Page 9

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QY      282 -TGDIS-----NMFEVAFCEGGMNNHAEFQSAKHGL 316
          | : |          | : |          | : |          |
DB      342 LRGGLTLDRDYGLNNIHNDI-----GTHVHILHLFQIRPHYHL 380

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Search completed: September 13, 2002, 09:49:22
Job time: 3742 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 08:51:00 ; Search time 43.85 seconds
(without alignments) 780.110 Million cell updates/sec

Title: US-09-664-840-2
Perfect score: 1946
Sequence: 1 LRSLVFPSTISLSLSLEAM.....ATNWKLPTEAOKIKAKSA 356
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	887.5	45.6	305	2	T52111
2	874.5	44.9	307	2	T52109
3	870.5	44.7	311	2	G84719
4	833	42.8	299	2	C86196
5	801	41.2	297	1	C61359
6	788.5	40.5	319	2	C86199
7	786.5	40.4	299	2	D86199
8	775.5	39.9	299	2	B86196
9	741	38.1	287	2	E86196
10	687	35.3	272	2	A17005
11	650	33.4	218	1	S75765
12	567.5	29.2	285	1	AC2429
13	556	28.6	278	1	S57643
14	423.5	21.8	479	2	T40925
15	402	20.7	493	1	S71634
16	359	18.4	451	1	UC6180
17	358.5	18.4	439	2	T28019
18	352	18.1	486	2	T18228
19	349.5	18.0	358	1	A24699
20	349	17.9	355	2	A32115
21	347.5	17.9	338	2	T28723
22	342.5	17.6	345	2	PC7092
23	338	17.4	476	2	S52746
24	329.5	16.9	333	2	T26230
25	329.5	16.9	358	1	A36507
26	326	16.8	510	1	S64059
27	324	16.6	397	2	F97707
28	319	16.4	395	2	F71711
29	215.5	11.1	237	2	I54779

30	206	10.6	392	2	F83610	probable fatty acyl
31	114	5.9	359	2	S52650	omega-3 fatty acid
32	111.5	5.7	404	2	Q03812	omega-3 fatty acid
33	108.5	5.6	446	1	J02336	omega-3 fatty acid
34	108.5	5.6	447	1	T43319	omega-3 fatty acid
35	105	5.4	380	2	T10898	Delta5 fatty acid
36	103	5.3	454	2	H88791	probable omega-3 f
37	102	5.2	377	2	B83454	protein T13P2.1 (l
38	101.5	5.2	359	2	AC2005	probable alkane hy
39	99.5	5.1	380	2	T06235	omega-3 fatty acid
40	99	5.1	460	2	T10063	omega-3 fatty acid
41	99	5.1	537	2	T51785	omega-3 fatty acid
42	98.5	5.1	438	2	T15039	lethal leaf-spot 1
43	95	4.9	514	2	B64634	omega-3 fatty acid
44	94	4.8	383	1	A44227	hypothetical prote
45	93.5	4.8	398	2	T01696	omega-3 fatty acid

ALIGNMENTS

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RESULT 1
T52111
stearyl-CoA desaturase (EC 1.14.99.5) ADS1 [imported] - Arabidopsis thaliana
N:Alternate names: delta 9 desaturase ADS1
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 31-Mar-2001
C:Accession: T52111
R:Pukuchl-Mizutani, M.; Tasaka, Y.; Tanaka, Y.; Ashikari, T.; Kusumi, T.; Murata, N.
Plant Cell Physiol. 39, 247-253, 1998
A:Title: Characterization of delta9 acyl-11lipid desaturase homologues from Arabidopsis
A:Reference number: 225959
A:Accession: T52111
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-305 <FUK>
A:Cross-References: EMBL:D88536; PDB:BAA25180.1
C:Genetics:
A:Gene: ADS1
C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 45.6%; Score 887.5; DB 2; Length 305;
Best Local Similarity 51.4%; Pred. No. 4.2e-72;
Matches 152; Conservative 53; Mismatches 88; Indels 3; Gaps 2;

QY 56 KQDLRRFRITSEVYLERKSKGFRMRKNPDIOMAVTLVLHALLAMAPFYFSWDAFWISF 115
DB 9 EENNKKMADAKEMGRKRAMERKRLDIYKAPASLFEVFLCLADPFNFTWPAALVAL 68

QY 116 ILGFASGVLTGTLGFHRCITGFGFKLPKIVEYFPAVCGSLAGDDEPMENSRINHOE 175
DB IV--YTVGGLGTVTSYHNHLAHSKPKWLEFFAYCGLATIDQDPIDWSTJRHVHOE 126

QY 176 VDEEDVHSPFOGFECHIGVLDKDLFEVRKGRNNVNDLKAQAFRLFQKTYMYHQ 235
DB 127 TDSDDPHSPNEGFEWSHILWLFDTGYLER--CGRRTVEDLKNQWYKFLQRIYVLIIL 185

QY 236 ALIALYLVGGPPYVWGMGRFLVPMFSTPAISVCKKMGCRWNNGDLSNNPVALC 295
DB 186 TFGFLIYFGGISFTWGMGLGVAMEHHVTLINSLCHVWGSRTWKNDYSRNWMLSVF 245

QY 296 AFEGGMHNNHAFDQASRHHGLEMMQIDVTYVITLQAGLATNVKLPTEAKOKKL 351
DB 246 SFGESWNNHHAFFSSARQGLEMMQIDISWITVAFLEILIGLATVKKLPESQRRRM 301

RESULT 2
T52109
stearyl-CoA desaturase (EC 1.14.99.5) [imported] - Arabidopsis thaliana
N:Alternate names: delta 9 desaturase
C:Species: Arabidopsis thaliana (mouse-ear cress)
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C:Date: 20-Oct-0000 #sequence_revision 20-Oct-2000 #text_change 20-Apr-2001
C:Accession: T52109
R:Fukuchi-Mizutani, M.; Tasaka, Y.; Tanaka, Y.; Ashikari, T.; Kusumi, T.; Murata, N.
Plant Cell Physiol. 39, 247-253, 1998
A:Title: Characterization of delta9 acyl-1-lipid desaturase homologues from Arabidopsis thaliana
A:Reference number: 225959
A:Accession: T52109
A:Status: preliminary; translated from GH/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-307 <FUK>
A:Cross-references: EMBL:D88537; PIDN:BAA25181.1
C:Genetics:
A:Gene: AD52
C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

[illegible]

RESULT 3
G84719
delta 9 desaturase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 20-Apr-2001
C:Accession: G84719
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, Y.; Koo, H.; Moffitt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Yamayam, L.; Tallent, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.; Title, Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420, MUID: 20083487
A:Accession: G84719
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-311 <STO>
A:Cross-references: GB:AE002093; NID:9458964; PIDN:AAD26482.1; GSPDB:GN00139
C:Genetic:
A:Gene: At2g31360
A:Map position: 2
C:Superfamily: mammalian stearoyl-CoA desaturase: stearoyl-CoA desaturase homology

	44.7%;	Score 870.5;	DB 2;	Length 311;
Query Match	51.9%;	Pred. No. 1.5e70;		
Best Local Similarity	Conservative 46;	Mismatches 88;	Gaps 3;	
Matches 152;				
OY	64	TSEVYLEKSKG--FWRRKKNNPDRQDQNAVTLVLALAAAFYSWDAFWSIFLLGRA	121	
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[illegible]

RESULT 4
C86196
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R:Accession: C66196
R:Author(s): A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Greasy, T.H.; Dewar
ansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucero, J.S.; Maitl, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A6141; MUID:21016719
A:Accession: C66196
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <STO>
A:Cross-references: GB:AE005172; NID:98810472; PIDN:AF80133.1; GSPDB:GN00411
C:Genetics:
A:Map position: 1
C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology

Query Match	Similarity	42.8%	Score	833	DB 2	Length	299
Best Local	Similarity	51.7%	Prod.	0.3	3.e-67		
Matches	153	Conservative	47	Mismatches	90	Indels	6
							Gaps
QY	56	KDDERERTSEVLEVERSKGFWRRKRNPRDIONAVTLVLHAAAPFYESWDAMISF	115				
		: : : : : : : : : : : : : : :					
Db	6	KDDSSSQKs---YRKERBAYLVLRKMTQFDVGRASTVGTVHLLCLLPANFYKMAEFFGI	62				
QY	116	ILLGPAASVGLITLCFPHRCLTHGFEKPKLVEYFFAFCGSLALOGDPMEMVSNRRYHOF	175				
		: : : : : : : : : : : : : : : : : : : :					
Db	63	ILALITN--LCITFSYHNHLTHRSFKLPKLEVEYFAASALLALOGDLDWVSHIRFHOF	120				
QY	176	VDTERDVHSPQGFECFHIGVWLKDLFEVKRGGRNNVNDLKAQAFYRFLOKTYMHOL	235				
		: : : : : : : : : : : : : : : : : : : :					
Db	121	TDSDRDPHSPIEGEWFESVLMIFPTD-YIRKCGRRNNVNDLKAQWYRFLKKTIVLHIL	179				
QY	236	ALIALLVYVGEPYIVMGGRFLVPMHSTFAINSVCHKMGKRPWNTGDISTNNMFALC	29				
		: : : : : : : : : : : : : : : : : : : :					
Db	180	AFWLIYILMGGLPYLTWVGVGGVIGYGTGLVNSACHICGSQAMQNDTSSRNWYMLAL	235				
QY	296	AFGECHNNHHNAFEDSARHGLEMMQIDVTWVIFTLQIGATVWKLPTFAOKOKL	351				
		: : : : : : : : : : : : : : : : : : : :					
Db	240	TMGESWNNHHAFAETISARHGLEMYOLDITWYLIWFPQALGLATWKLPLTDQKKRM	295				

RESULT

8
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
A:Accession: E86196
R:Theologas, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Hutzler, L.

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L., Jenkins, J., Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.-H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Malil, R.; Marshall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Title: Sequence number: AB6141; MWID:21016719
A:Reference number: AB6141; MWID:21016719
C:Genetics:
A:Map position: 1
C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology

Query Match 39.9%; Score 775.5; DB 2; Length 299;
Best Local Similarity 51.8%; Pred. No. 4,8e+62;

Matches 145; Conservative 37; Mismatches 95; Indels 3; Gaps 2;

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19 ERKAEFFRKMTRIDARASVAGVAHLCLLAPFNKWALRGVLAIVT--LSITFTSY 76
132 HKCFLNGFKRLCKLYEYFAYCGSLATGDDPEWYSNNRYHNHFQVDTERDVSPTQGFWF 191
77 HNLTHTSKRLPKWLLEYPRAYSALFPALOGHPIDWSTHRFHNFQSDRDPSPIEGFWF 136
192 CHIGVNLDKDLFEVKGRGNRVNDLKQAFRFLQTMYMHQLAILLLTYVGSPRIY 251
137 SHVFIFDPDYIAREKGG-RDNVMIDLKOEWEPFLNRTGLTHILFWTLVWGSGLPYLTVT 195
252 WGMGFELVPWFNSTFAINSVCCHKMGCRPWNTGDLTNNMVALCAFGSWMNHNAFBQS 311
Db CGAVGVGTGYNGTWLNINACHINGSRAMNTKDTSRNIMWLGSPFMGSMMHHAFAS 255
OY ARHGLEMWDIVWTVIYIRTLQATGLATNYKKLFTEAKOKKL 351
Db ARHGLEMWQVDLVWLIICFCFOALGIATDVTKLPDTAKORKL 295

RESULT

9
E86196
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
A:Accession: E86196
R:Theologas, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Hutzler, L.

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.-H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Malil, R.; Marshall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MWID:21016719
A:Accession: E86196
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-267 <STO>

A:Cross-references: GB:AE005172; NID:g8810474; PIDN:AAF80135.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1
 C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology

```

Query Match          38.1%; Score 741; DB 2; Length 287;
Best Local Similarity 47.0%; Pred. No. 5,8e-59;
Matches 140; Conservative 44; Mismatches 96; Indels 18; Gaps 5;

OY 54 KKKDLERFRISSEVYLERKSKGFRKKNRPDIQNAVTLVLVHAAAPFFESDAAWI 113
    ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 4 KKKDDSS--SOSKAVRKKRAFLRKTRVDVMVNSAAGAHLLCLAPFNYWEARF 60
    ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
OY 114 SPILLGFASGVYGLTLCFRCILTHGGFKLPKLYEFFYVCGSLALQDPMEMVSNHRYH 173
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 61 A-AMVGISIN-LSITFSYIRNLTHRSFKLPKLEYPFALSALFALQGDPIDWSTYHREH 118
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
OY 174 QFVDTERDVHSPFGWFECHIGVWLDKLFEVKGGRNNVNDLKKQAFYRLOTTYH 233
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 119 QETDSRDHSPHSEGGWFESHVFIPTSYIRKCGG-RNNVNDLQQMFYRLOTTYH 177
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
OY 234 QALATLLAYVGGFPIYVWGMGRFLYFMHSFFAINSYCHKKGRRPMTGDLSTNNMFA 293
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 178 ILTFWILVYLWGLPILWVSGVGAIGYHAIWLINSACHIMGSAAKMTKDISRIIMWIG 237
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
OY 294 LCAFGEGNNHNAFEQSARHGLEWMDIDVTYVIRTLOAGLATNVKLPTEAOKRL 351
    ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 238 PFTMGESWNNHNAFEASARHGLEWYQ-----LGLADVYKLPTDAOKRM 283
    ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||

RESULT 10
AI2005
delta-9 desaturase [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AI2005
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iriq,
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AI2005
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <CUR>
A:Cross-references: GB:BA000019; PIDN:BA877965.1; PID:g17135419; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:  

A:Gene: desc
C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology
```

Query Match 35.3%; Score 687; DB 2; Length 272;
 Best Local Similarity 47.6%; Pred. No. 3.9e-54;
 Matches 128; Conservative 48; Mismatches 73; Indels 20; Gaps 4;

```

OY 88 NAYTLVLVH--ATAAMPFFESMDAFWISFILLGFASGVYGLTLCFHRCLTHGGFKLPKL 145
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 15 NTLFPLGLHIGALFAFLPSNFSMAAVGA-LLLYWTIGGAGITLGFRLYTHRSFQTPKW 73
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
OY 146 VEEFFAYVCGSLALQDPMEMVSNHRYHNOVDTERDVHSPFGWFECHIGVWL----- 198
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 74 LEVFLVGLCTGACGGRPEVWGTNRHNLHSDRDPDHNKSGFMWSHIMLLYHSPESA 133
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
OY 199 DKDLFEVKGGRNNVNDLKKQAFYRLOTTYHNOALATLLAYVGGFPIYVWGMGFR 258
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
DB 134 DVPRFTK-----DIEDPYQFLQTYFTITQALGILLLYLGGMSFYVWGMGFR 163
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||

259 VFMSHFFAINSYCHKKGRRPMTGDLSTNNMFAALCAFGEGNNHNAFEQSARHGLEW 318
    : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
184 VMVYHGTMLVNSATNFKFGYRTYDAGDSTNCMVVAVLVEFGSWNNHNAFEQSARHGLEW 243
```

OY 319 WQIDVTVVIRTLQALIGLATNVKLPTEAO 347
 DB 244 WEVDLTWMTVOLQILGLATNVKLPTEAO 272

RESULT 11

S57565

stearyl-CoA desaturase (EC 1.14.99.5) 1 - *Synechocystis* sp. (strain PCC 6803)
 N:Alternate names: acyl-CoA desaturase 1; delta9 fatty acid desaturase; protein sll0541
 C:Species: *Synechocystis* sp.
 A:Variety: PCC 6803
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 R:Kanezo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shlimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, N. Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
 A:Reference number: S74322; MID:97061201
 A:Accession: S57565
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-318 <RAN>
 A:Cross-references: EMBL:D64003; GB:AB001339; NID:91001200; PIDN:BA10500.1; PID:9100125
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:gene: des9
 C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology
 C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
 F:95-278/Domain: stearyl-CoA desaturase homology <SDH>

Query Match 33.4%; Score 650; DB 1; Length 318;
 Best Local Similarity 45.5%; Pred. No. 9, 8e-51;

Matches 116; Conservative 48; Mismatches 87; Indels 4; Gaps 2;

OY 91 TELVLNALAMAPFYSDMAFWISFILLGASVGLTLCFHNCLTHGFGKLPKLYEYF 150
 DB 61 TSHLVALLALFLPQFSWKAAGVAFLLYITGCT-CITLGFHNCISHRSEFNPWKLEYLF 119
 OY 151 AYCGLALODPMEVSNHRYHQFVDERDVHSPTOGFMECHIGVLDKDLFEVGRGR 210
 DB 120 VICGTACOGGVEWVGLHNMHNFSDTPRPHDSKGFWMHSLIGMME--IPAKAI 176
 OY 211 RNVNNDLKAQAFRLOKTYMYQLLALLLVYVCGPPTVWGMGRVLPFMRHSTPAINS 270
 DB 177 PRYTKDIDDKFYQFQCNLLILQVALGLILFALGMPVINGIEFVRLVFEHFTWVNS 236
 OY 271 VCHKMGSRPMNTGDLSTNNMFVALCAFGEGMNNHNAFQSGARHGLEMMQIDVTWTVRT 330
 DB 237 AFHKFGYVSHESNDYSRNCMMVALLFLFGGMNNHNAIYOSARHGLQMEVDLWMTIKF 296
 OY 331 LQALIGLATNVKLPTE 345
 DB 297 LSLGLAKDKLPPE 311

RESULT 12

AG3429

delta-9 desaturase [Imported] - *Anabaena* sp. (strain PCC 7120)
 C:Species: *Anabaena* sp.
 A:Note: *Anabaena* sp. (strain PCC 7120) is a synonym of *Nostoc* sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
 C:Accession: AG3429
 R:Kanezo, T.; Nakamura, Y.; Molt, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shlimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AG3429
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-285 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA876690.1; PID:917134129; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:gene: desC
 C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology

Query Match 29.2%; Score 567.5; DB 2; Length 285;

Best Local Similarity 37.6%; Pred. No. 2, 3e-43;
 Matches 103; Conservative 58; Mismatches 92; Indels 21; Gaps 5;

OY 78 RRRKNPRDIONAVTLVLNALAMAPFYSDMAFWISFILLGASVGLTLCFHNCLTH 137
 DB 17 RLSTW-----NVAFTTIALALAPFWFSWALGL-LFLPLMFGSICICGYNRLSH 70
 OY 138 GGGKLPKLYEYFPAACGSLALODPMEVSNHRYHQFVDERDVHSPTOGFMECHIGV 196
 DB 71 KSFQVPMKLEVAIVATIGALAMOGGPIFGVHGRHNAHTEVDYLDPRYSQGRFWSHML 130
 OY 197 VL-----DKDLFEVGRGRNNVNDLKAQAFRLOKTYMYQLLALLLVYVCGPPT 249
 DB 131 ILTPRESEFYDEY-----QVAPDLAROPPYRMLDRYFILLQIPGLMLYALGWSF 183
 OY 250 IYWGMEFLVFMFHTFALNSVCHKMGSRPMNTGDLSTNNMFVALCAFGEGMNNHNAFE 309
 DB 184 VYIGVVLRAVLLMHSWTFVNSATHHMGYRTFNADNARLMMVSLVTVGEGHNNHHTYR 243
 OY 310 QSARHGLEMMQIDVTWTVRTLQALIGLATNVKLP 343
 DB 244 NVAKAGFQWMEVDYTWMSIKLDTLGLAKKVL 277

RESULT 13

S57643

stearyl-CoA desaturase (EC 1.14.99.5) - *Synechococcus* sp.
 N:Alternate names: Delta9 fatty acid desaturase
 C:Species: *Synechococcus* sp.
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jun-2000
 C:Accession: S57643
 R:Nishizawa, O.; Toguri, T.
 submitted to the EMBL Data Library, January 1994
 A:Description: Fatty acid desaturase gene from *Anacystis nidulans*.
 A:Reference number: S57643
 A:Accession: S57643
 A:Molecule type: DNA
 A:Residues: 1-278 <NIS>
 A:Cross-references: EMBL:X77367; NID:9886832; PIDN:CA54556.1; PID:9886833
 A:Note: the source is designated as *Anacystis nidulans*
 C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology
 C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
 F:54-243/Domain: stearyl-CoA desaturase homology <SDH>

Query Match 28.6%; Score 556; DB 1; Length 278;
 Best Local Similarity 40.1%; Pred. No. 2, 4e-42;

Matches 108; Conservative 52; Mismatches 83; Indels 26; Gaps 6;

OY 89 AVTLVLNLH--ALAMAPFYSDMAFWISFILLGASVGLTLCFHNCLTHGFGKLPKLY 146
 DB 16 ALFPAVAILIGLALLFLPQFSWKAAGVAFLLYITGCT-CITLGFHNCISHRSEFNPWK 74
 OY 147 EYFPAACGSLALODPMEVSNHRYHQFVDERDVHSPTOGFMECHIGVLDKDLFEVGR 199
 DB 75 EYVLVFCGTLAMQGRILEWIGLHNNHLSQDDVDHNSKGFPLMSHFLMAYITPAKTE 134
 OY 200 KDLFEVGRGRNNVNDLKAQAFRLOKTYMYQLLALLLVYVCGPPTVWGMGRVLPFMR 253
 DB 135 VDKF-----TRIDAGDPVYRFFNKYFFQVOLLGLVLLYAMGBAWGNGMSFYVMG 184
 OY 254 MGRFLVFMFHTFALNSVCHKMGSRPMNTGDLSTNNMFVALCAFGEGMNNHNAFQSGAR 313
 DB 185 IFARLVVVYVHTVLYNSATIKFGYRSHESGDSQSTNCMMVALLFLFGGMNNHNAIYOSAR 244

OY 314 HGLEWQIDVTWYVIRTLQALGATNKL 342
 D 245 HGLQWMEFDLWLIIGLKKVGLARKIKV 273

RESULT 14

T40925 stearyl-CoA desaturase (EC 1.14.99.5) SPCC1281.06c [similarity] - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000

C:Accession: T40925
 R:Voickert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, January 1999

A:Reference number: Z21957

A:Accession: T40925

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-479 <VOL>

A:Cross-references: EMBL:AL035218; PIDN:CAA22827.1; GSPDB:GN00068; SPDB:SPCC1281.06c

A:Experimental source: Strain 972h-; cosmid c1281

C:Genetics:

A:Gene: SPDB:SPCC1281.06c

A:Map position: 3

C:Superfamily: yeast stearyl-CoA desaturase; cytochrome b5 core homology; stearyl-CoA

C:Keywords: heme; iron; metalloprotein; oxidoreductase

F:104-294/Domain: stearyl-CoA desaturase homology <SDH>

F:390,416/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 21.8%; Score 423.5; DB 2; Length 479;

Best Local Similarity 30.4%; Pred. No. 3.6e-30;

Matches 106; Conservative 62; Mismatches 142; Indels 39; Gaps 10;

OY 19 AMASLTATTPAMPAPASVLD--PKIPKPEPKTEPRKPDLEFRFRTSEVVLERRSKG 75
 D 6 AAFASATQPTTEGNASMKRTIPVPSPERKWDPRKHIOQDPWMO-----N 57
 OY 76 FRRR-KMNRDIONAVTLVLHALAMAPFYSMDAFNISFLLGFAAGVGLITLCFHNK 134
 D 58 WNRHLNW-----LRCHLIGLPMIALYGVFTTPILOTKILIFAIYYAASGLITGYNHL 112
 OY 135 LTHGFKLPLKLYEYFFAYGSLAOGDPMEVSNHRYHHQVDEEDVHSPLOGFCHT 194
 D 113 WSRAYKAKKPLEYFLAAGCAAFEGSIRWMSRDRHNRKYDTDKDPYNAKGFYAHV 172
 OY 195 GWVLDKDLFEVRRGGRNNVNDLKKQAEFRLOKTYMHOALLILLYVGGEPR---I 250
 D 173 GWTI---ILQNPRIIGRSVSDLSNDFVEMNHR---HFLPIASPMFT--FPSLFGCL 223
 OY 251 VWC---MGF-----RLVPMFHSFPAINSVCHKMGGRPWNTGDLSTNNMFVALCAFGEGM 301
 D 224 LMWDYRGYFYAGVCLVYVNHATFCVNSLANLIGSQPFDDTNSARNHFTALVTLGEGN 283
 OY 302 HNNHNAFEQSARHGLEWQIDVTWYVIRTLQALGATNKLPTLEAKOK 350
 D 284 HNYHNAFPDYNRGLRWYEDPTKIFITYASLFLGLAYNLNTEPDMEIOK 332

RESULT 15

S71634 stearyl-CoA desaturase (EC 1.14.99.5) - Cryptococcus curvatus

N:Alternate names: Delta9 fatty acid desaturase

C:Species: Cryptococcus curvatus

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: S71634

R:Meesters, P.A.E.P.; Eggink, G.

Yeast 12, 723-730, 1996

A:Title: Isolation and characterization of a Delta-9 fatty acid desaturase gene from the

A:Accession: S71634

A:Molecule type: DNA

A:Cross-references: EMBL:Y10422; NID:g1783356; PIDN:CAA71449.1; PID:g1783357
 A:Experimental source: strain CBS570
 C:Genetics:
 A:Gene: OLE1
 C:Superfamily: yeast stearyl-CoA desaturase; cytochrome b5 core homology; stearyl-CoA
 C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosyn
 F:119-308/Domain: stearyl-CoA desaturase homology <SDH>
 F:372-448/Domain: cytochrome b5 core homology <CBS>
 F:406,432/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 20.7%; Score 402; DB 1; Length 493;

Best Local Similarity 28.9%; Pred. No. 3.2e-28;

Matches 109; Conservative 60; Mismatches 124; Indels 84; Gaps 12;

OY 9 ISISLSLEAMASFIAITTPAMPAPASVLDPKIPKPEPKTEPRKPDLEFRFRTSEVVL 68
 D 1 MSASTATPPPTAPAVANPTPAAASAAA---APAAITKKAETIDES--EIFVVS--- 51
 OY 69 LERKSGFWRRKKNPRDIONAVTLVLHALAMAPFYFS--MDAEWISF----- 115
 D 52 -----QNVVTRFV--ENMTMLPPVTVSMILQNIOWISFTALTVPAPMA 92
 OY 116 -----ILLGFASGVGLITLCFIRCLTHGFKLPLKLYEYFFAYGSLAL 158
 D 93 IYGLCTLELOKRTYIMAIYVYFMFG-LGITAGYHRLAHNRYNASADLYFLALCGAGSV 151
 OY 159 QGDPMENVSNNRYHNOFVDEEDVHSPLOGFCHIGVLDKDLFEKRGG-RRNNVNDL 217
 D 152 QGSIKWMSRGHRAHRTYDTKLDIPYSAHEGFWMAHVGMML-----VAPRGKIGVADISDL 206
 OY 218 KKQAFYRFLQKTYMHOLALIALIYYGGEPRYIWMGKF-----RLVPMFHS 264
 D 207 SRNPVYKWOHNKY---VMLAVYLMGLV--FPTLVAAGLGMGDKGLLPAGAARLVFVHHS 260
 OY 265 TFAINSVCHKMGGRPWNTGDLSTNNMFVALCAFGEGMNNHNAFEQSARHGLEWQIDVT 324
 D 261 TFCVNSLANHMLGETPFDKHTPKDHFITALVTVGEGIHNFHIOFPMDFRNAIKRYQYDPT 320
 OY 325 WYVIRTLQALGATNKL 341
 D 321 KMFITMKNVGLASHLK 337

Search completed: September 13, 2002, 09:50:27
 Job time: 3567 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:49:24 ; Search time 24.91 Seconds

(without alignments)
553.358 Million cell updates/sec

Title: US-09-664-840-2

Perfect score: 1946
Sequence: 1 LRSLVPPISISLSLEAM.....ATNVKLPPEAKOKLAKKSA 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349.5	18.0	358	1 ACOD_RAT	P07308 ratius norv
2	346	17.8	355	1 ACOD_MOUSE	P13516 mus musculu
3	344.5	17.7	359	1 ACOD_SHEEP	O62849 ovis aries
4	343.5	17.7	334	1 ACOD_PIG	O02858 sus scrofa
5	343.5	17.7	359	1 ACOD_BOVIN	O91694 bos taurus
6	342	17.6	354	1 ACOD_MESAU	O64420 mesocricetu
7	331.5	17.0	359	1 ACOD_HUMAN	O00767 homo sapien
8	329.5	16.9	358	1 ACOD_MOUSE	P13011 mus musculu
9	326	16.8	510	1 ACOD_YEAST	P21147 saccharomyc
10	111.5	5.7	404	1 FD3C_BRANA	P46310 brassica na
11	108.5	5.6	446	1 FD3C_ARATH	P46310 brassica na
12	105	5.4	380	1 FD3C_PNAU	P32291 phaseolus a
13	99	5.1	460	1 FD3C_RICCO	P48619 ricinus com
14	98.5	5.1	447	1 FD3C_SBSIN	P48622 arabidopsi
15	95.5	4.9	435	1 FD3C_ARATH	P48624 brassica na
16	94	4.8	383	1 FD32_BRANA	P48624 brassica na
17	92.5	4.8	759	1 PMT6_YEAST	P42934 saccharomyc
18	91.5	4.7	530	1 MATP_HUMAN	O9umk9 homo sapien
19	90	4.6	377	1 FD31_BRANA	P46311 brassica na
20	90	4.6	453	1 FD3C_SOYBN	P48621 glycine max
21	89.5	4.6	369	1 XYLM_PSEPU	P21395 pseudomonas
22	89	4.6	330	1 RCENL_ERKSP	P26279 erythrobact
23	88.5	4.5	635	1 S6A8_BOVIN	O18875 bos taurus
24	88	4.5	975	1 PMPA_CHLTR	O84417 chlamydia t
25	87.5	4.5	1394	1 CNG4_BOVIN	O28181 bos taurus
26	86	4.4	1411	1 Y297_HUMAN	O15040 homo sapien
27	85.5	4.4	635	1 S6A8_RAT	P28501 rattus norv
28	84	4.3	213	1 AMIS_MYCSM	P56583 mycobacteri
29	84	4.3	386	1 FD3E_ARATH	P48623 arabidopsi
30	83	4.3	389	1 O85C_DROME	O9vh66 drosophila
31	82	4.2	515	1 TLG1_CHLUP	O92812 chlamydia p
32	81.5	4.2	530	1 MATP_MOUSE	P58335 mus musculu
33	81.5	4.2	635	1 S6A8_HUMAN	P48029 homo sapien

34	80.5	4.1	329	1 COX3_ACACA	O37374 acanthamoeb
35	80.5	4.1	426	1 S6A8_HUMAN	P53796 homo sapien
36	80	4.1	1672	1 PMPA_CHLMD	O9pij2 chlamydia m
37	79.5	4.1	379	1 FD3E_TOBAC	P48626 nicotiana t
38	78.5	4.0	262	1 COX3_ANOQU	P33508 anopheles q
39	78.5	4.0	461	1 CDS1_HUMAN	O92903 h phosphati
40	78	4.0	709	1 FZD6_MOUSE	O61089 mus musculu
41	77.5	4.0	327	1 ENF2_MOUSE	O61672 m equilibra
42	77.5	4.0	418	1 EF1G_ORYSA	O92117 oryza sativ
43	77.5	4.0	476	1 MM10_HUMAN	P09238 homo sapien
44	77.5	4.0	909	1 CNG4_HUMAN	O14028 homo sapien
45	77	4.0	410	1 Y588_BUCAL	P57648 buchnera ap

ALIGNMENTS

RESULT 1
ACOD_RAT ID ACOD_RAT STANDARD; PRT; 358 AA.
AC P07308;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl-CoA desaturase (EC 1.14.99.5) (Stearyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase).
GN SCD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=87008535; PubMed=2428815;
RA Thiede M.A., Ozols J., Strittmatter P.;
RT "Construction and sequence of cDNA for rat liver stearyl coenzyme A desaturase.";
RT J. Biol. Chem. 261:13230-13235(1986).
RL J.
CC - FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEARYL-COA DESATURASE SYSTEM. THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA AND STEAROYL-COA.
CC - CATALYTIC ACTIVITY: Stearyl-CoA + AH(2) + O(2) -> oleoyl-CoA + A + 2 H(2)O.
CC - COFACTOR: IRON.
CC - SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Probable).
CC - INDUCTION: THIS PROTEIN IS THE ONLY INDUCIBLE COMPONENT OF THIS FATTY ACYL-COA DESATURASE SYSTEM.
CC - DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/OR BE INVOLVED IN METAL ION BINDING.
CC - MISCELLANEOUS: DESATURASE HAS A HALF-LIFE OF ONLY 4 HOURS.
CC - SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
CC EMBL: J02585; AAA42116.1; -.
CC PIR: A24699; A24699.
CC InterPro: IPR001522; Desaturase.
CC Pfam: PF01069; Desaturase.1.
CC PRINTS: PR00075; FACDSATPRASE.
CC ProDom: PD002221; Desaturase.1.
CC PROSITE: PS00476; FATTY-ACID-DESATUR.1.
CC OxiReductase; Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum; Iron.
CC TRANSMEM 75 95 POTENTIAL.

FT TRANSMEM 97 117 POTENTIAL.
 FT TRANSMEM 221 241 POTENTIAL.
 FT TRANSMEM 314 334 POTENTIAL.
 FT DOMAIN 119 124 HISTIDINE BOX 1.
 FT DOMAIN 156 160 HISTIDINE BOX 2.
 FT DOMAIN 297 301 HISTIDINE BOX 3.
 SO SEQUENCE 358 AA: 41483 MW: EEC960B111D62F0C CRC64;

Query Match 18.0%; Score 349.5; DB 1; Length 358;
 Best Local Similarity 26.3%; Pred. No. 3.9e-23;
 Matches 93; Conservative 70; Mismatches 146; Indels 45; Gaps 10;

QY 18 EAMASEFIATTPAMPAPASVLDPKIPTKPEP-----KTEPKKDDL-ERRTSEVLEERK 72
 DB 8 EISSYTTTITTEPPSGNLNGRKKMKVPLYLEDIHPEREDIHDPYQDEEGPPPK 67
 QY 73 SKGFRRKRNPRDIONAVTLVLH-----LAAMPFFSDAFWISFLLGFASGV 124
 DB 68 LEYVWR-----NIIIMALLHVALGYLITLPPSKYVTLMGIFY-----YLISA 111
 QY 125 LGITLGHRCILTHGGEKLPKLYEYEFAYCGSLALOGDPMENWSNHRHHQFVDTREDVHS 184
 DB 112 LGITGAHRLNHSRTYKARLPRLITLANTWAFQNDYEWARDRHAKHKESETHADPHN 171
 QY 185 PTQGFQFCHIGWVL-DKDLFEYKRGGRNNVNDLKKQAFYRFLQKTYMHQIALIALLY 243
 DB 172 SRGFFSFHVGWLVLRKHPAVKEGKGL-DMSDLKAELKLVMEQRR---YKRGILLMCFI 227
 QY 244 VGGF-PLYVNGMF-----RLVFMHSTFAINSVCHKGGRPNNTGDLSTNNMFV 292
 DB 228 LPTLVPMYCWGETFLHSLFVSTFLKTYTLVLANTWLVNSAHLXYGRPDKNIOSRENILV 287
 QY 293 ALCAFGEGMNNHNAFESARHGLEWMOIDYTWYIRFLQALIGLATNYKLPTPEA 346
 DB 288 SLGSGEGEFHNYHNAFPDYDASAEYRWMIHNTFTTFIDCMALGLAVDRKKVSKA 341

RESULT 2
 ACOD_MOUSE STANDARD; PRT; 355 AA.
 ID ACOD_MOUSE
 AC P13516;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ACYL-CoA desaturase 1 (EC 1.14.99.5) (Stearoyl-CoA desaturase 1)
 DE (Fatty acid desaturase 1) (Delta(9)-desaturase 1).
 GN SCD1
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adipocyte;
 RX MEDLINE=89034247; PubMed=2903162;
 RA Ntambi J.M., Buhrow S.A., Kaestner K.R., Christy R.J., Sibley E.,
 RT Kelly T.J. Jr., Lane M.D.;
 RT "Differentiation-induced gene expression in 3T3-L1 preadipocytes.
 RT Characterization of a differentially expressed gene encoding
 RT stearoyl-CoA desaturase.";
 RT J. Biol. Chem. 263:17291-17300(1988).
 RL J. Biol. Chem. 263:17291-17300(1988).
 CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEARYL-COA
 CC DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED
 CC CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
 CC SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA
 CC AND STEAROYL-COA.
 CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) = oleoyl-CoA + A +
 CC 2 H(2)O.
 CC -1- COFACTOR: IRON.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Probable).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE

AND/OR BE INVOLVED IN METAL ION BINDING.
 -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; M21285; AAA40103.1; JOINED.
 DR EMBL; M21280; AAA40103.1; JOINED.
 DR EMBL; M21281; AAA40103.1; JOINED.
 DR EMBL; M21282; AAA40103.1; JOINED.
 DR EMBL; M21283; AAA40103.1; JOINED.
 DR EMBL; M21284; AAA40103.1; JOINED.
 DR PIR; A32115; A32115.
 DR MGI; MGI:98239; Scd1.
 DR InterPro: IPR001522; Desaturase.
 DR Pfam; PF01069; Desaturase; 1.
 DR PRINTS; PR00075; FRCDDSATRASE.
 DR PRODOM; PD002221; Desaturase; 1.
 DR PROSITE; PS00476; FATTY_ACID_DESATUR_1; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Multigene family;
 KW Transmembrane; Endoplasmic reticulum; Iron.
 FT TRANSMEM 72 92 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT TRANSMEM 219 239 POTENTIAL.
 FT TRANSMEM 311 331 POTENTIAL.
 FT DOMAIN 116 121 HISTIDINE BOX 1.
 FT DOMAIN 153 157 HISTIDINE BOX 2.
 FT DOMAIN 294 298 HISTIDINE BOX 3.
 SO SEQUENCE 355 AA: 41000 MW: BB586E2B23228E44 CRC64;

Query Match 17.8%; Score 346; DB 1; Length 355;
 Best Local Similarity 27.7%; Pred. No. 7.7e-23;
 Matches 96; Conservative 76; Mismatches 150; Indels 32; Gaps 11;

QY 18 EAMASEFIATTPAMPAPASVLDPKIPTKPEKTE--TPPKDDL-ERRRSEVLEERKSK 74
 DB 8 EISSYTTTITITAPPSGNERE-KVKTVPRLHEEDIRPEMEDIHDPYQDEEGPPKLE 66
 QY 75 GFWRRKRNPRDIONAVTLVLAALAAAPFYF--SWDAFWISFLLGFASVIGITTCFH 132
 DB 67 YVWR-----NIIIMALLHVALGYLITLPPSKYVTLMGIFY-----YLISA 116
 QY 133 RCLTHGFEKLPKLYEYEFAYCGSLALOGDPMENWSNHRHHQFVDTREDVHSPTQGFQF 192
 DB 117 RUMSHRTYKARLPRLITLANTWAFQNDYDWARDRHAKHKESETHADPHNSRGFFS 176
 QY 193 HIGWVL-DKDLFEYKRGGRNNVNDLKKQAFYRFLQKTYMHQIALIALLYVGGF-PYI 250
 DB 177 HVGWLVLRKHPAVKEGKGL-DMSDLKAELKLVMEQRR---YKRGILLMCFIPLTPVMY 232
 QY 251 VMGGMGF-----RLVFMHSTFAINSVCHKGGRPNNTGDLSTNNMFVALCARGEG 300
 DB 233 CWGETFANSLFVSTFLKTYTLVLANTWLVNSAHLXYGRPDKNIOSRENILVSLGAVGEG 292
 QY 301 WHNNHNAFESARHGLEWMOIDYTWYIRFLQALIGLATNYKLPTPEA 346
 DB 293 FHNHHTFPFDYSASEYRWMIHNTFTTFIDCMALGLAVDRKKVSKA 338

RESULT 3
 ACOD_SHEEP STANDARD; PRT; 359 AA.
 ID ACOD_SHEEP
 AC 062849;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ACYL-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty

DE acid desaturase) (Delta(9)-desaturase).

GN SCD.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID:9940;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Y1089; TISSUE-Adipose tissue;

RA MEDLINE-98223428; PubMed-9554990;

RA Ward R.J., Travers M.T., Richard S.E., Vernon R.G., Salter A.M.,

RA Buttery P.J., Barber M.C.;

RT Stearoyl-CoA desaturase mRNA is transcribed from a single gene in the

RT ovine genome.

RT Blochlin. Biophys. Acta 1391:145-156(1998).

CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEAROYL-COA

CC DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED

CC CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A

CC SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA

CC AND STEAROYL-COA (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) -> oleoyl-CoA + A +

CC 2 H(2)O.

CC -1- COFACTOR: IRON.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic

CC reticulum (Probable).

CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE

CC AND/OR BE INVOLVED IN METAL ION BINDING.

CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: A001048; CAA04502.1; -

DR InterPro: IPR001522; Desaturase.

DR Pfam: PF01069; Desaturase: 1.

DR PRINTS: PR00075; FACDSATRASE.

DR Prodom: PD002221; Desaturase: 1.

DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.

KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane;

KW Endoplasmic reticulum; Iron.

FT TRANSMEM 76 96 POTENTIAL.

FT TRANSMEM 98 118 POTENTIAL.

FT TRANSMEM 223 243 POTENTIAL.

FT TRANSMEM 315 335 POTENTIAL.

FT DOMAIN 120 125 HISTIDINE BOX 1.

FT DOMAIN 157 161 HISTIDINE BOX 2.

FT DOMAIN 302 302 HISTIDINE BOX 3.

SO SEQUENCE 359 AA; 41671 MW; 219CFBBIJE35418 CRC64;

Query Match 17.7%; Score 344.5; DB 1; Length 359;

Best Local Similarity 27.4%; Pred. No. 1,1e-22;

Matches 101; Conservative 56; Mismatches 144; Indels 67; Gaps 11;

QY 15 LSLFMASTIATTTTPMPAFASVLD-----PKIP-----TKPPK-----TET 52

DB 6 LQBEISSSTTTTITAPP-SVYLDNGGKLEKTPLYEEDIRPMRDIDYDPNQDEG 64

QY 53 PKPKDLEFRTESEVLLERKSGFWRKRNPRDIONAVTLVLALAL-----AMAFYFSW 108

DB 65 PKPK-----LEV-----VVR-----NIIIMGLHGLXGTLIPTCIY 99

QY 109 DAFWISFILGFASGVLTITCFHRCILTHGFKLPKLYEPFACGSLALOGDPNFWNSN 168

DB 100 TFLMWLFY---YVISALGLTIGVHRLMSHRYKARLPRLVLIANTMAFONDVEFMSRD 156

QY 169 HRYHQFQVTERDVHSPTOGEWFCIGVLDKDLFVEKRGGRNNVNDLKKQAFYRFLQK 228

DB 157 HRAHKKFSETDADPHNSRRGFESHGWLVRKHPAVREKGAITLDSLRAEKLVAFQR 216

QY 229 TYMYHOLATLALYYVGGFYIWMGMF-----RLVMEHSTPLINSCHWGR 278

DB 217 YKRGVLLCFILPTL--VPWYLMGESFONSLEFATPLKRAVLANFTWLSAAHMYGYR 274

QY 279 PMNTGDLSTNNMFVALCAREGHNHNAFEQSARGLEMMQIDVTWYVIRFLQALGLAT 338

DB 275 PYKRTNPRENILVSLGAVGEFHNHTFPYDSASEYRWHINFTTFIDCAALIGLAY 334

QY 339 NVKLPTFA 346

DB 335 DRKKVSKA 342

RESULT 4

ACOD_PIG ACOD_PIG STANDARD; PRT; 334 AA.

AC 002858;

DT 15-JUL-1998 (rel. 36. Created)

DT 15-JUL-1998 (rel. 40. Last sequence update)

DT 16-OCT-2001 (rel. 40. Last annotation update)

DE Acyl-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty

DE acid desaturase) (Delta(9)-desaturase) (Fragment).

GN SCD.

OS Sus scrofa (pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID:9623;

RN [1]

RP SEQUENCE FROM N.A.

RA Fumiere O.;

RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEAROYL-COA

CC DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED

CC CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A

CC SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA

CC AND STEAROYL-COA (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) -> oleoyl-CoA + A +

CC 2 H(2)O.

CC -1- COFACTOR: IRON.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic

CC reticulum (Probable).

CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE

CC AND/OR BE INVOLVED IN METAL ION BINDING.

CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL: Z97186; CAB10004.1; -

DR InterPro: IPR001522; Desaturase.

DR Pfam: PF01069; Desaturase: 1.

DR Prodom: PD002221; Desaturase: 1.

DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.

KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane;

KW Endoplasmic reticulum; Iron.

FT NON_TER 1 1

FT TRANSMEM 65 85 POTENTIAL.

FT TRANSMEM 87 107 POTENTIAL.

FT TRANSMEM 212 232 POTENTIAL.

FT TRANSMEM 304 324 POTENTIAL.

FT DOMAIN 109 114 HISTIDINE BOX 1.

FT DOMAIN 146 150 HISTIDINE BOX 2.

FT DOMAIN 287 291 HISTIDINE BOX 3.

FT NON_TER 334 334

SO SEQUENCE 334 AA; 38482 MW; 79183E3918469977 CRC64;

Query Match 17.7% Score 343.5; DB 1; Length 334;
 Best Local Similarity 28.3%; Pred. No. 1.2e-22;
 Matches 99; Conservative 64; Mismatches 144; Indels 43; Gaps 13;

21 ASFTATTPPAMPAPASVLD-----DPKIPPKPEKPTPKPKDOL--ERRRSEVLEERK 72
 1 SSVYTTTTTTPAS-SRYLONGGKSEKTPQYVEDIR-PEKKDIDYDPTQDEKGP-QGK 57

73 SKGWRKRNPRDIONAVTLVLHALA---AMAPFFSMDAF-ISFILLGFAVGLGI 127
 58 LEYWR-----NIIIMSLHLGALYGLITLPTCKYITLLMAFAYLL-----SAVG 104

128 TLCEFRCLTHGGFKLPKLYEYFAVCGSLALGDPMEVSNHRYHQFDTERDVSPTQ 187
 105 TAGAHRMSHTYKARLEPLRFELIANTMAQNDYEMARDBRAHNFSESDADPHNSRR 164

188 GFWRCHIGWVL-DKDLVEYKRGRRNNVNDLKOAFYFLQKTYMYQIALIALLYVGG 246
 165 GFESHSVGMVLVRRKHPAVEKGGLL-NMSDKAKELVNFORRYKPGILLMCFILPTI-- 221

247 FRYIYWGSGF-----RLVFMHSTFAINSYCHKMGGRPNNTGDLSTNNMFALCA 296
 222 VPMTCWGAEPFOSLFVATFLKAYLANTWLVNSAHLXGRPYDKTISPRENILLVSLGA 281

297 FGEGRNNHNAFEQSARHGLEWMOIDVTWYVIRLQALGATNVKLPTEA 346
 282 VGEGFHNHYHFFPYDYSASEYRMHINTLTFEIDCMAALGLAYDRKAKVSKA 331

RESULT 5
 ACOD_BOVIN STANDARD; PRT; 359 AA.

AC 09PT94;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acyl-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase).
 GN SCD.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=adipose tissue;
 RA Chung M.I., Ha S.H., Baik M.G., Choi Y.J.;
 RT "Cloning and characterization of full-coding cDNA of bovine stearoyl CoA desaturase from adipose tissue."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEARYL-COA DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA AND STEAROYL-COA (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) = oleoyl-CoA + A + 2 H(2)O.
 CC -1- COFACTOR: IRON.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Probable).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC EMBL: AF186710; AAF22305.1; -
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FADDSATPASE.
 DR Prodom: PD002221; Desaturase; 1.
 DR PROSITE: PS00476; FATTY ACID DESATUR-1; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane;
 KW Endoplasmic reticulum; Iron.
 FT TRANSMEM 76
 FT TRANSMEM 98
 FT TRANSMEM 223
 FT TRANSMEM 315
 FT TRANSMEM 335
 FT DOMAIN 120
 FT DOMAIN 157
 FT DOMAIN 161
 FT DOMAIN 296
 FT DOMAIN 302
 FT SEQUENCE 359 AA; 41755 MW; 22FB69FBD1846C33 CRC64;

Query Match 17.7% Score 343.5; DB 1; Length 359;
 Best Local Similarity 28.3%; Pred. No. 1.3e-22;
 Matches 104; Conservative 52; Mismatches 145; Indels 67; Gaps 11;

15 LSLFAMASFIATTTTPAMPAPASVLD-----PKIP-----TKPEK-----TET 52
 6 LQEISSSYTTTTTTPAP-SRYLONGGKLEKTPYLEEDIRPEKRDIDYDPTQDEK 64

53 PKRPDDELRRTSVVLEERSKSGFWRKRNPRDIONAVTLVLHALA---AMAPFFSM 108
 65 PKPK-----LEY-----VWR-----NIIIMSLHLGALYGLITLPTCKIY 99

109 DAFWISFILLGFAVGLITLCEFRCLTHGGFKLPKLYEYFAVCGSLALGDPMEVSN 168
 100 TYIVLFFYYL---MGALGITAGAHRLMSHRTYKARLEPLRFELIYGMFAMQNVFEMSRL 156

169 HRYHQFDTERDVHSPQGFWRPCHIGWVL-DKDLVEYKRGRRNNVNDLKOAFYFLQK 228
 157 HRAHNFSESDADPHNSRRGFESHSVGMVLVRRKHPAVEKGGSTLNSDLAEKLVNFQR 216

229 TYMYHQLALILLYYGGFPIYVGMGRFLVFMF-----HSTFAINSYCHKWGR 278
 217 YKRGVILLCFILPTL--VPMYLMDETFONSLEFATLEFRYALGANTWLVNSAHLMYGYR 274

279 FWNFGDLSTNNMFYALCAFGSGMNNHNAFEQSARHGLEWMOIDVTWYVIRLQALGAT 338
 275 PYDKTINPRENILLVSLGAVGEGFHNHYHFFPYDYSASEYRMHINTLTFEIDCMAALGLAY 334

339 NVKLPTEA 346
 335 DRKAKVSKA 342

RESULT 6
 ACOD_MESAU STANDARD; PRT; 354 AA.

AC 064420;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acyl-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase).
 GN SCD OR FAR-17C.
 OS Mesocricetus auratus (golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95290467; PubMed=7772580;
 RA Ideta R., Seki T., Adachi K.;
 RT "Sequence analysis and characterization of FAR-17C, an androgen-

```

RT dependent gene in the flank organs of hamsters."
CC J. Dermatol. Sci. 9:94-102(1995).
CC
CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEAROYL-COA
CC DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED
CC CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
CC SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA
CC AND STEAROYL-COA (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: stearyl-CoA + AH(2) + O(2) = oleoyl-CoA + A +
CC 2 H(2)O.
CC -1- COFACTOR: IRON.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Probable).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L26956; AAC42058.1; -
CC DR InterPro: IPR001522; Desaturase.
CC DR Pfam: PF01069; Desaturase; 1.
CC DR PRINTS: PR00075; FADDSATRASE.
CC DR PRODOM: PD002221; Desaturase; 1.
CC DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
CC DR Oxidoreductase; Fatty acid biosynthesis; Transmembrane;
CC KM Endoplasmic reticulum; Iron.
CC FT TRANSMEM 71 91 POTENTIAL.
CC FT TRANSMEM 93 113 POTENTIAL.
CC FT TRANSMEM 218 238 POTENTIAL.
CC FT TRANSMEM 310 330 POTENTIAL.
CC FT DOMAIN 115 120 HISTIDINE BOX 1.
CC FT DOMAIN 152 156 HISTIDINE BOX 2.
CC FT DOMAIN 293 297 HISTIDINE BOX 3.
CC SO SEQUENCE 354 AA; 40968 MW; B41A0B31845EB874 CRC64;

Query Match 17.6%; Score 342; DB 1; Length 354;
Best Local Similarity 26.9%; Pred. No. 1.7e-22;
Matches 98; Conservative 61; Mismatches 141; Indels 64; Gaps 13;

QY 15 LSLKAMASTIATTTTPAMPAPASYLDKIP-----TKRPK-----TETPKKD 58
DB 6 LQEMTSTYTTTTTTPPESEIAQTVLYLEEDIRPEKEDIYPSYQDEGPPK-- 63
QY 59 LERFRTSEVVLKRSKGFRRKRNPNRDIONAVTLVLALALA-----AMAPFTSMDAFWIS 114
DB 64 -----LEY---VVR-----NIIMALHLGALYGLVLPSSKYYTLIM-A 99
QY 115 FILLGASVGLGTLICFHGCLTHGFKLPKLYEYFPAVCGSIALOGDPMEVSNHRYHHO 174
DB 100 FYV--YVIEIGAGVHMLMSHRTYKALPLRIFILINTAMAFQNDYEMARDHAHAK 157
QY 175 FVDTEDVHSPTQGEWFEGHIGVYL-DKDLFVEKRGRRNNVNDLKKQAFRYFLQKTYMH 233
DB 158 FSETYADPHDSRGFFSHVGMVLVYRKHPAVEKGGKL-DMSDLKNEKLYMQR---Y 213
QY 234 QIALIALLLVYVCGF-PYIWMGFM-----RLVFPFHSFPAINSYCHKMGKGPWNT 282
DB 214 KPAILLMCYTLPLFVFWYWGAEFVNSLCVSTFLRYTLVLTWLVNSAAHLGYRPPYDK 273
QY 283 GDLSTNMFVALCAGFEGGNNHNAFEQASARHGLEWMOJDVWYVYRTQALGTLNVL 342
DB 274 NIDPRNALVSLGCLGEGHNHNAFPPYDYSASBYRMHINFTTFIDCAALGLATDRKK 333
QY 343 PTEA 346
DB 334 VSKA 337

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RESULT 7
ID ACOD_HUMAN STANDARD; PRT; 359 AA.
AC 000767; Q16150; Q9Y695;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty
DE acid desaturase) (Delta(9)-desaturase).
GN SCD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RA Al-Jeyan L., Mccord A., Pierotti A.R., Craft J.A.;
RA Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver, Brain, and Skin;
RA MEDLINE=99247918; PubMed=10229681;
RA Zhang L., Ge L., Parimoo S., Steen K., Prouly S.M.;
RA "Human stearyl-CoA desaturase: alternative transcripts generated from
RA a single gene by usage of tandem polyadenylation sites."
RA Biochem. J. 340:255-264(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Hoshino T., Ohtsu K.;
RA "Cloning, sequencing and expression of human stearyl-CoA
RA desaturase."
RA Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 3-239 FROM N.A.
RC TISSUE=adipose tissue;
RC MEDLINE=94222609; PubMed=7909540;
RC Li J., Ding S.-F., Habib N.A., Fermor B.F., Wood C.B., Gilmour R.S.;
RC "Partial characterization of a cDNA for human stearyl-CoA desaturase
RC and changes in its mRNA expression in some normal and malignant
RC tissues."
RC Int. J. Cancer 57:348-352(1994).
RL
RL -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEAROYL-COA
RL DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED
RL CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
RL SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA
RL AND STEAROYL-COA.
RL -1- CATALYTIC ACTIVITY: Stearyl-CoA + AH(2) + O(2) = oleoyl-CoA + A +
RL 2 H(2)O.
RL -1- COFACTOR: IRON.
RL -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
RL reticulum (Probable).
RL -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
RL AND/OR BE INVOLVED IN METAL ION BINDING.
RL -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
RL
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RL
RL EMBL: Y13647; CAA73998.1; -
RL EMBL: AF097514; AAD29870.1; -
RL EMBL: AB032261; BAA93510.1; -
RL EMBL: S70284; AAB30631.1; -
RL MIM: 604031; -
RL InterPro: IPR001522; Desaturase.
RL Pfam: PF01069; Desaturase; 1.

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DR PRINTS: PR00075; FACDSATBASE.
DR PRODOM: PD002221; Desaturase; 1.
DR PROSITE, PS00476; FATTY_ACID_DESATUR_1; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane;
KW Endoplasmic reticulum; Iron.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 98 118 POTENTIAL.
FT TRANSMEM 223 243 POTENTIAL.
FT TRANSMEM 315 335 POTENTIAL.
FT TRANSMEM 120 125 HISTIDINE BOX 1.
FT DOMAIN 157 161 HISTIDINE BOX 2.
FT DOMAIN 298 302 HISTIDINE BOX 3.
FT CONFLICT 5 5 L -> M (IN REF. 4).
FT CONFLICT 8 8 D -> E (IN REF. 4).
FT CONFLICT 25 26 PG -> SR (IN REF. 2 AND 3).
FT CONFLICT 25 26 M -> L (IN REF. 2 AND 3).
FT CONFLICT 224 224 F -> C (IN REF. 4).
FT CONFLICT 237 237 N -> T (IN REF. 2 AND 3).
FT CONFLICT 320 320 W -> C (IN REF. 2 AND 3).
FT CONFLICT 326 326 T -> A (IN REF. 2 AND 3).
FT CONFLICT 333 333
SQ SEQUENCE 359 AA; 41559 MW; 2FC8BF6023ACA2F0 CRC64;

Query Match 17.0%; Score 331.5; DB 1; Length 359;
Best Local Similarity 26.1%; Pred. No. 1.4e-21;
Matches 93; Conservative 60; Mismatches 147; Indels 57; Gaps 11;

QY 21 ASPLATPPAPAPASVADPKIPKPEKTEP-----PKPKDL--ERFRTSEV 68
DB 12 SSIYTTTTITP-----PQVLONGGDKLTMPLYLEDDIRPDIKDITPTTYKDKGP 65
QY 69 LEKSKGFWRRKRNPRDIONAVTLVLH-----ALAAPFY-FSDAFWISFLLGF 120
DB 66 -SPKVEYVWR-----NIIIMSLHLGALYGITLIPCKEYFWLMGVFY-----Y 108
QY 121 ASGVLTLCRHCLTHGCGFKLPKLYEFPAFCGSLAQSPMEVNSHRRHNOVDTER 180
DB 109 FVSALGITAAGAHRLMSHSYKARLPRLRLFLIANTMAQONVYEWARDRAHNKFETHA 168
QY 181 DVHSPTGCFWFCCHIGVLDKDLFEVRCGRNRNVNDLKKQAFYRLOKTYMHQALAL 240
DB 169 DPHNSRGFFFSHVGWMLVLRKHPAVKEGSLDLSDAEKLYVQGR---YKKGLLMM 225
QY 241 LYYVGF-PIYVWGMF-----RLVFMFSTFAINSVCNKGGRPMWTDGLSTNN 289
DB 226 CFILPTLVFWVEGETFQNSVFATFLRYAVVLAATWLVSAAHLFGYRPYDKNISPREN 285
QY 290 MFVALCAGEBGMNNHNAFEGSARHGLEMWQIDVTWYVIRLQALGATNVKLPTEA 346
DB 286 ILVSLGAVGEGHNHNSFPYDYSASEYRWHINFTFFIDWMAALGLTYDRKKVSKA 342

RESULT 8
AC02_MOUSE STANDARD: PRT: 358 AA.
ID AC02_MOUSE
AC P13011;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl-CoA desaturase 2 (EC 1.14.99.5) (Stearoyl-CoA desaturase 2)
DE (Fatty acid desaturase 2) (Delta(9)-desaturase 2).
CN SC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipocyte;
RX MEDLINE=89359271; PubMed=2570068;
RA Kaestner K.H., Ntambi J.M., Kelly T.J., Lane M.D.;
RT "differentiation-induced gene expression in 3T3-L1 preadipocytes. A
RT second differentially expressed gene encoding stearoyl-CoA

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RT desaturase.*;
RL J. Biol. Chem. 264:14755-14761(1989).
CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEARYL-COA
CC DESATURASE SYSTEM. THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED
CC CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
CC SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA
CC AND STEAROYL-COA.
CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) = oleoyl-CoA + A +
CC 2 H(2)O.
CC -1- COFACTOR: IRON.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Probable).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
CC EMBL, M26270; AAA4094.1; -.
CC DR PIR: A36507; A36507.
CC DR MGD: MGI:98240; SC2.
CC DR InterPro: IPR001522; Desaturase.
CC DR Pfam: PF01069; Desaturase; 1.
CC DR PRINTS: PR00075; FACDSATBASE.
CC DR PRODOM: PD002221; Desaturase; 1.
CC DR PROSITE, PS00476; FATTY_ACID_DESATUR_1; 1.
CC KW Oxidoreductase; Fatty acid biosynthesis; Multigene family;
CC KW Transmembrane; Endoplasmic reticulum; Iron.
FT TRANSMEM 75 95 POTENTIAL.
FT TRANSMEM 97 117 POTENTIAL.
FT TRANSMEM 222 242 POTENTIAL.
FT TRANSMEM 314 334 POTENTIAL.
FT DOMAIN 119 124 HISTIDINE BOX 1.
FT DOMAIN 156 160 HISTIDINE BOX 2.
FT DOMAIN 297 301 HISTIDINE BOX 3.
SQ SEQUENCE 358 AA; 41073 MW; 201904F1F1262A9F CRC64;

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Query Match 16.9%; Score 329.5; DB 1; Length 358;
Best Local Similarity 28.9%; Pred. No. 2.1e-21;
Matches 90; Conservative 55; Mismatches 133; Indels 33; Gaps 9;

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QY 53 PKPRDDL--ERFRTSEVLEKSKGFWRRKRNPRDIONAVTLVLHMLA---AMAPYF 106
DB 47 PELKDDLDVPTDYDDEGP-PRKLEYVWR-----NIIIMALHLGALYGITLVP--- 93
QY 107 SMDAFWISFLLGFASGVLTGCFHRCITGCGFKLPKLYEFPAFCGSLAQDPMENV 166
DB 94 SCKLYTCLFAVLLYYTSLATAGAHRLMSHRYKARLPRLRLFLIANTMAQONVYEW 153
QY 167 SNHRHNOFVPTDERDVHSPPTGFWFCCHIGVLDKDLFEVRCGRNRNVNDLKKQAF 225
DB 154 RDHRAHNKFESEHDAPHNSRGFFFSHVGWMLVLRKHPAVKEGGL-DMSDLKKEKLV 212
QY 226 LOKTYMHQALILALLYVVGGPYVWGMF-----RLVFMFSTFAINSVCNKG 275
DB 213 ORRYKPKDLLMCEVLPPL--VPKTCWGEFTVNSICVSTFLRYAVVLAATWLVSAA 270
QY 276 GGRPMWTDGLSTNNFVALCAGEBGMNNHNAFEGSARHGLEMWQIDVTWYVIRLQAL 335
DB 271 GYRPYDKNISRENILVSMGAVGERFHNYHNAFPYDYSASEYRWHINFTFFIDCMALL 330
QY 336 LATNVKLPTEA 346
DB 331 LAYDRKRVSR 341

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RESULT 9
ACOL_YEAST STANDARD: PRT: 510 AA.
ID ACOL_YEAST
P21147;
AC 01-MAY-1991 (Rel. 18, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl-CoA desaturase 1 (EC 1.14.99.5) (Stearoyl-CoA desaturase 1)
GN (Fatty acid desaturase 1).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Saccharomycetes: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes:
OC Saccharomycetales: Saccharomycetaceae: Saccharomyces.
NCBI_Taxid=4932;
RX MEDLINE-91056050; PubMed-1978720;
RA Stuker J.E., McDonough V.M., Martin C.E.;
RT "The Urel gene of Saccharomyces cerevisiae encodes the delta 9 fatty
RT acid desaturase and can be functionally replaced by the rat stearyl-
RT CoA desaturase gene."
RT J. Biol. Chem. 265:20144-20149(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97377993; PubMed-9234674;
RA Feuerhahn M., de Montigny J., Potler S., Souciet J.-L.;
RT "The characterization of two new clusters of duplicated genes
RT suggests a 'Lego' organization of the yeast saccharomyces cerevisiae
RT chromosomes."
RT Yeast 13:861-869(1997).
RL -1- FUNCTION: UTILIZES O(2) AND ELECTRONS FROM THE REDUCED CYTOCHROME
CC B(5) DOMAIN TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
CC SPECTRUM OF FATTY ACYL-CoA SUBSTRATES (PROBABLE).
CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) -> oleoyl-CoA + A +
CC 2 H(2)O.
CC -1- COFACTOR: IRON.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Probable).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -1- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
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CC -----
DR EMBL: J05676; AAA34826.1; -
DR EMBL: 272577; CAA96757.1; -
DR PIR: A23675; A23675.
DR SGD: S0003023; OLE1.
DR InterPro: IPR001139; Cyt_LB5.
DR InterPro: IPR001522; Desaturase.
DR Pfam: PF01069; Desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00075; FADDSATURASE.
DR ProDom: PD002221; Desaturase; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS00255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
KM Oxidoreductase; Fatty acid biosynthesis; Iron; Electron transport;
KM Transmembrane; Endoplasmic reticulum; Heme.
FT TRANSMEM 113 133 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 236 276 POTENTIAL.
FT TRANSMEM 281 301 POTENTIAL.
FT DOMAIN 161 166 HISTIDINE BOX 1.
FT DOMAIN 198 202 HISTIDINE BOX 2.

FT DOMAIN 335 339 HISTIDINE BOX 3.
FT DOMAIN 409 487 HEME-BINDING.
FT BINDING 444 444 HEME LIGAND (BY SIMILARITY).
FT BINDING 470 470 HEME LIGAND (BY SIMILARITY).
FT CONFLICT 304 304 L -> M (IN REF. 1).
SQ SEQUENCE 510 AA; 58403 MW; A6CC78DD4210ECCA CRC64;

Query Match 16.8%; Score 326; DB 1; Length 510;
Best Local Similarity 29.5%; Pred. No. 6.3e-21;
Matches 83; Conservative 50; Mismatches 114; Indels 34; Gaps 8;

QY 97 ALAAMPFYSSNAPFISFLILGFASVGLITICFPHCLTHGKFLPKLYEFPATCGSL 136
DB 130 ALGKVPFLHNVLELFYSFY---YAVGVSITGAYHRLMHSRSYSAHPRLFLFATGCA 185
QY 157 ALGGDPMEVSNRHYHOFEDTERDVSPGQMFEGICGVLLKDEVEKGRGRNVND 216
DB 186 SVGSAKMGHSHRHHRYDTLRDPDARGLMYSMGMLKP---NPKYARADYTD 242
QY 217 LKQAFYRFLQKTYMYHQI-----ALIALY---YVGGEPIYWGMRFLVFMF-HST 265
DB 243 MTDDWTIRFQHRHYILLMLTAFVYPTLCGYFFENDYMGGLY---AGTIRFVIGQAT 298
QY 266 FAINSCHKMGGRPMNTGDTNNMFALCAFGEGMNNHAEQSRHGLEMMQIDYTW 325
DB 299 FCINSLAHYIGTGFEDRRTPTDNTAIVTFEGYHNFHEPPTDYRNAIKMYOYDPTK 358
QY 326 YVIRTLQALIGLANNVK-----LPTAKOG-KLKAK 354
DB 359 VVILNLSVLADLKLKFSQNALIEALIQOEOKINKKKK 399

RESULT 10
FD3C_BRANA STANDARD: PRT: 404 AA.
ID FD3C_BRANA
AC P48618;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-)
DE (Fragment).
GN PAD7
OS Brassica napus (Rape).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
OC eurosid II: Brassicales; Brassicaceae; Brassica.
OX NCBI_Taxid=3708;
RN RN
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RA MEDLINE-94302147; PubMed-8029334;
RA Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
RA Kinney A.J., Hitz W.D., Booth J.R., Jr., Schweitzer B., Stecca K.L.,
RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
RA Feldman K.A., Pierce J., Browne J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases."
RT Plant Physiol. 103:467-476(1993).
RL -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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DR EMBL: L22963; AAA61774.1; ALT_INIT.

DR PIR: P00812; P00812.

DR InterPro: IPR001225; FA_desaturase.

DR Pfam: PF00487; FA_desaturase; 1.

DR ProDom: PD001081; FA_desaturase; 1.

KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;

KW Transf. peptide.

FT NON_TER 1

FT TRANSIT 1

FT CHAIN ?

FT DOMAIN 121 404 OMEGA-3 FATTY ACID DESATURASE.

FT DOMAIN 157 161 HISTIDINE BOX 1.

FT DOMAIN 324 328 HISTIDINE BOX 3.

SO SEQUENCE 404 AA; 46617 MW; 4B58FB2F36E2ED4 CRC64;

Query Match 5.7%; Score 111.5; DB 1; Length 404;

Best Local Similarity 23.6%; Pred. No. 0.022;

Matches 83; Conservative 44; Mismatches 98; Indels 127; Gaps 27;

OY 43 PTKPEPKTE-----TPKPKDLERRTSEVLEKRS--KGFWRKRNPRDIONAVT--LL 93

DB 36 PLEEDPKTORPDGAPPP-----FNLDI---RAIPKHCWK--NPKMSYVVRRLA 84

OY 94 VHAALAAAPF---YESMDAFWISFLILGASGVIGITLCRCILHGGF-----KLKPIY 146

DB 85 IYFALAGAAIYNNWLVPLIAGIYFWALFVLG---HDC-GHGFSMDPRINSVY 138

OY 147 EYFAYCGSLALQDPMEMVSNHRYHQ---FVDERDVH-----SPTGFWFC 192

DB 139 GHLLSSILVPHYG---WRISHRTHQHGHWENDESMHPSSEKITYSLDKPTPFREF 194

OY 193 -----HIGWVL-----DKDLPEKRGGRNNVNDLKKQAFYFLQKITYY 232

DB 195 LPLVLAAYPYLIWARSPEKKGSHYHDSDLFLPK---ERNVD-----LITSTACW 240

OY 233 HOLA-LIALIYVVG-----PPY---IYWGMGFRLVFEHSTFAINSVCHK----- 274

DB 241 TAMAVLVLICINLVNPMQMLKIYLPYMINVM-LDF-VTYIHNG-----HEDKLPW 291

OY 275 WGRFPMW--TGDLST-----NNMEVALCAFEGEGHNNHAFQOSARHGL 316

DB 292 YRGKEMSYLRGGLTTLDRDYGLINNIIHDI-----GTIVIHLLFPQIPHYHL 338

RESULT 11

FD3C_ARATH STANDARD; PRT; 446 AA.

AC P46310;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE 01-MAR-2002 (Rel. 41, Last annotation update)

DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).

GN FAD7 OR FAD7 OR AT3G11170 OR F9F8.4 OR F11B9.10.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliopsida; core eudicots; Rosidae;

OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV, COLUMBIA; TISSUE=Hypocotyl;

RX MEDLINE=94302147; PubMed=8029334;

RA Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,

RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,

RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,

RA Feldmann K.A., Pierce J., Browne J.,

RT "Cloning of higher plant omega-3 fatty acid desaturases.";

RL Plant Physiol. 103:467-476(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV, COLUMBIA; TISSUE=Aerial parts;

RX MEDLINE=94043239; PubMed=8226956;

RA Iba K., Gibson S., Nishuchi T., Fuse T., Nishimura M., Arondel V.,

RA Hugly S., Somerville C.R.;

RT "A gene encoding a chloroplast omega-3 fatty acid desaturase

RT complements alterations in fatty acid desaturation and chloroplast

RT copy number of the fat7 mutant of Arabidopsis thaliana.";

RL J. Biol. Chem. 268:24099-24105(1993).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=CV, COLUMBIA; TISSUE=Hypocotyl;

RL Watabiki M., Yamamoto K.;

RN Submitted (NOV-1993) to the EMBL/Genbank/DBJ databases.

RC STRAIN=CV, COLUMBIA;

RX MEDLINE=21016720; PubMed=11130713;

RA Salanoubat M., Lemcke K., Rieger M., Ansoerg W., Unsel M.,

RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,

RA Delzeny M., Boutry M., Grivell L.A., Maché R., Puigdomenech P.,

RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,

RA Winkler P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Verzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,

RA Corrad A., Hornischer K., Kauer G., Loehner T.-H., Nordick G.,

RA Reichelt J., Schärfe M., Schoen O., Barues M., Terol J., Climent J.,

RA Navarro P., Collado M., Berger-Llauro C., Purrello B., Masuy D.,

RA Cooke R., Laudie M., Beyer-Llauro C., Purrello B., Masuy D.,

RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,

RA Monfort A., Argitrou A., Flores M., Lignori R., Vitale D.,

RA Mannhaupt G., Haase D., Schoof H., Rüd S., Zaccaria P., Wewes H.-W.,

RA Rooney T., Kizuo M., Wats A., Uteback T., Fujii C.Y., Jenkins J.,

RA Creasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,

RA Pail G., Miltischer J., Sellers P., Gill J.E., Felblyum T.V.,

RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,

RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,

RA Watanabe A., Yamada M., Yasuda M., Tabata S.;

RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis

RT thaliana.";

RL Nature 408:820-822(2000).

CC -I- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES

CC THE THIRD DOUBLBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY

CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT

CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS

CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.

CC -I- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.

CC -I- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

CC -I- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.

CC -I- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE

CC AND/ OR BE INVOLVED IN METAL ION BINDING.

CC -I- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

CC -----

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CC -----

DR EMBL: L22961; AAA61774.1; -

DR EMBL: D14007; BAA03106.1; -

DR EMBL: D26019; BAA05040.1; -

DR EMBL: AC009991; AAF01508.1; -

DR EMBL: AC073395; AAG50977.1; -

DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desaturase; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KW Transit peptide.
 FT TRANSIT 1 2 CHLOROPLAST (POTENTIAL).
 FT CHAIN 1 2 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 163 167 HISTIDINE BOX 1.
 FT DOMAIN 199 203 HISTIDINE BOX 2.
 FT DOMAIN 366 370 HISTIDINE BOX 3.
 SQ SEQUENCE 446 AA; 51174 MW; 121125f634553035 CRC64;

Query Match 5.6%; Score 108.5; DB 1; Length 446;
 Best Local Similarity 22.0%; Pred. No. 0.045;
 Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;

QY 1 LRSLKFPISISLSLEMAAF-----IATTP-AMPAASVLDKPIPKPEPKETEK 54
 DB 36 LSSSTKSTSSPLSGFNSHOGFTRMALMVSTPLTPPLF-----ESPL 80
 QY 55 PKDLERFRTSEV-----VLERKSKGFV-RRKMP-----RDIONAVTLVLAALAM 101
 DB 81 EEDNKQRFDPGAPRPENLADIRAIPIKCKVKNPKMSLSVYRDV-----AIVFALAG 134
 QY 102 APF---YFSWDAWISFILGFRASGVLTLCRHRLTHGCF---KLPLVEYFAYCG 154
 DB 135 AALNWMIVPRLVLAOGTFMALFVLG-----HDC-GHGSFENDKLKLSVGHLSHSI 188
 QY 155 SLALOGDPMKWNVSNHRYHNO---FVDERDVH-----SPDGRMFC----- 192
 DB 189 LVPIYHG---WRISHTHQNHNHGHVNDENSHMPSKIKNTLDKPRFRFRLPLVLMAY 244
 QY 193 -HIGWV-----DKDLFEVERKGRNNVNDLKOAFYRFLQKTYMHOA--LI 238
 DB 245 PFYLMARSPGKSGHYHPSDLELPK---ERKDV-----LTSTACMTAMALLV 290
 QY 239 ALLYVG-----GFRY---IYWGMRFLVPMFSTALNSVCKK-----WGRPMN- 281
 DB 291 CLMFTTGPITMLKLYGIPWINVM-LDF-VYULHNG-----HEDKLPWYRKEMSY 341
 QY 282 -TGDIST-----NNMFVALCAFGEGMNNHAFEOSARHGL 316
 DB 342 LRGGLTLTLDYGLINNIHNDI-----GTHVHHLFRLPHNYL 380

RESULT 12
 FD3E_PHAU
 ID FD3E_PHAU STANDARD; PRT: 380 AA.
 AC P32291;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-)
 DE (Indole-3-acetic acid induced protein Arg1).
 GN ARG1.
 OS Phaseolus aureus (mung bean) (Vigna radiata).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 OX NCBI_TaxID=3916;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=hypocotyl;
 RA Yamamoto K.T., Mori H., Imaseki H.;
 RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
 RT elongating hypocotyls of mung bean (Vigna radiata).";
 RL Plant Cell Physiol. 33:13-20(1992).
 CC -1- FUNCTION: MICROSMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPROVING THE FLAVOR OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER

CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- INDICATION: BY AUXIN, ETHYLENE AND WOUNDING.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -----
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DR EMBL: D14410; BAA03306.1; -
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desaturase; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KW Transmembrane.
 FT TRANSMEM 59 78 POTENTIAL.
 FT TRANSMEM 208 231 POTENTIAL.
 FT TRANSMEM 238 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX 1.
 FT DOMAIN 133 137 HISTIDINE BOX 2.
 FT DOMAIN 300 304 HISTIDINE BOX 3.
 SQ SEQUENCE 380 AA; 43996 MW; 1C005117A8DAE168 CRC64;

Query Match 5.4%; Score 105; DB 1; Length 380;
 Best Local Similarity 21.6%; Pred. No. 0.076;
 Matches 77; Conservative 38; Mismatches 105; Indels 136; Gaps 21;

QY 36 SYLDEKIPK---PEPKTPRKDLEFRFRTSEVLEKSKGEMRRKNPDIONAVTL 92
 DB 20 SYFDGAPPPFKIADIRAIPIKHCSEKSTLSLSYL-----BDV----- 59
 QY 93 LVILHALMAA---PYFSMDAIFISFILGFRASGVLTLCRHRLTHGCF---KLPL 145
 DB 60 LVYTLAASAIISFNKSTFPLYPAGOGTFMALFVLG-----HDC-GHGSFSSSKLSNF 113
 QY 146 VEYFAYCGSLALOGDPMKWNVSNHRYHNO---FVDERDVHSPDGRMFC---LDKDLF 203
 DB 114 VGHILSLTLVPYNG---WRISHTHQNHNHGHVNDENSHMPSKIKNTLDKPRFRFRLPHNYL 157
 QY 204 VEKRGGRNNVNDLKKOAFYR-----FLQKTYMHO----- 234
 DB 158 -----KNLDDMTMLRYSPPPIFAVRYFLMNRSPGKSGHNPYSNLFSPGERKV 209
 QY 235 -----LALIALLYY---VG-----GPRYIYWGMRFLVPMFSTALNSVCKK- 274
 DB 210 VSTLCKGIVLSVLXLSLTITGPITMLKLYGYPYLIYFVWMLDFYULNH---HGYTHYL 265
 QY 275 -WGRPMN--TGDISTNNMFVALCAFGEGMNN-----HNAEOSARHGL 316
 DB 266 PMYRQOEMSYLGLTLYDR-----DYGWNNVNHDIQTHVHHLRPHNYL 314

RESULT 13
 FD3C_RICCO
 ID FD3C_RICCO STANDARD; PRT: 460 AA.
 AC P48619;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
 DE FAD7A-1.
 GN Ricinus communis (Castor bean).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiales; Ricinus.

```

OX NCBI_Taxid=3988;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, BAKER 296; TISSUE=seed;
RX MEDLINE=94302177; PubMed=8029360;
RA van de Ioo F.J.; Somerville C.R.;
RT "Plasmod omega-3 fatty acid desaturase cDNA from Ricinus communis.";
RL Plant Physiol. 105:443-444(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L25897; AAA73511.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.
DR ProDom: PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Translt peptide.
FT CHAIN 1 ? ? CHLOROPLAST (POTENTIAL).
FT DOMAIN 177 181 HISTIDINE BOX 1.
FT DOMAIN 213 217 HISTIDINE BOX 2.
FT DOMAIN 380 384 HISTIDINE BOX 3.
FT SEQUENCE 460 AA; 52561 MW; 836592904EF3C7B0 CRC64;
SQ
Query Match 5.1%; Score 99; DB 1; Length 460;
Best Local Similarity 20.8%; Pred. No. 0.31;
Matches 75; Conservative 42; Mismatches 106; Indels 138; Gaps 19;
OY 52 TPKPDDLEERTSEVLEKSKGFWRRKWP-----RDIONAV----- 90
DB 76 TVSGDDDEREFNGIVNDEKGEFFDAGAPPTLADIRAIKHKCVKMPWMSMY 135
OY 91 --TLVLNALAAMPFYSSWDA---FWISFLLGFASGYLGITLCHRCRLTHGFG---K 141
DB 136 LRDVVVVGGLAAVAAYFNNWVAMPPLWFCQGTMFVALFVLG-----HDC-GHGSFSNNPK 189
OY 142 LKLEYEYFAVCGSLADGDPMEWVSNHRYHQ--FVDTEDVHSPGQFV----- 190
DB 190 LNSVGHLLHSITLYPHG---WRISRTTHQNHGHVENDSMHPLSEKITYKSLDNTK 245
OY 191 -----FCHIGWL-----DKDLFEVEKRGRRNNVNDLKKQAFYRELQ 227
DB 246 TLRFSLPPLMAYPRYLMSRSPGKGSHPHDSGLFVPR-----ERKDI-----IT 291
OY 228 KTYMTHQALALLLYVG-----GPPYIWMGSGFLVWMEHSTFAINSYCHK- 274
DB 292 STACW--TAMALLVLYLNFSGMPVOMLKLXGIPYWIIFWMLDFEVLH-----HHG 340
OY 275 -----MGGRPMN--TGDLSTNNMFVALCARGEGMHNH-----HHAFEQSARHG 315
DB 341 HEDKLPMTRGKMSYLRGGLTLDR-----DYGMINNHHIDIGTNYIHLLFPQIPRYH 393
OY 316 L 316
DB 394 L 394

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RESULT 14
FD3C_SESIN STANDARD; PRT; 447 AA.
AC P48620;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
GN FAD7.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_Taxid=4182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, 4294; TISSUE=Cotyledon;
RA Shoji K.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
DR EMBL; U25817; AAA70334.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.
DR ProDom: PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Translt peptide.
FT CHAIN 1 ? ? CHLOROPLAST (POTENTIAL).
FT DOMAIN 167 171 HISTIDINE BOX 1.
FT DOMAIN 203 207 HISTIDINE BOX 2.
FT DOMAIN 370 374 HISTIDINE BOX 3.
FT SEQUENCE 447 AA; 51116 MW; 4E76250DD6DA6B1 CRC64;
SQ
Query Match 5.1%; Score 98.5; DB 1; Length 447;
Best Local Similarity 22.3%; Pred. No. 0.33;
Matches 79; Conservative 31; Mismatches 101; Indels 143; Gaps 23;
OY 43 PTKRPKTEPRKPDLEERTSEVLEKSKGFW-RRKWP-----RDIONAVTLVLH 96
DB 94 PGAPRP-----FKLSD-IRRAIPKHKCVKMPWMSGYVADV-----AVVF 133
OY 97 ALAAMAAPFYFS--WDATWISFLLGFASGYLGITLCHRCRLTHGFG---KLPKYVEYF 149
DB 134 GLAAVAAYFNNWVAPPLWFCQGTMFVALFVLG-----HDC-GHGSFNDPKLNSVGH 187
OY 150 FAYCGSLADGDPMEWVSNHRYHQ--FVDTEDVH-----KLPKYVEYF 183
DB 188 LHSITLYPHG---WRISRTTHQNHGHVENDSMHPLSEKITYKSLDNTATKRLFLPLF 243
OY 184 -----SP-TGQFWFCHIGWLDKDLFEVEKRGRRNNVNDLKKQAFYRELQ 230
DB 244 PLLAVIYLMRSRPGKGSHP-H-----PDSDLFVYNE-----KKDVIYTVCWTA 288

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OY 231 MYHOLALIALLYVG-----GPPYIWMGKGFRLVMEFSTRAINSVCHK----- 274
 DB 269 ML--ALLVGLSPVIGRPVOLLKLYGIPYLGNYWMDLYLH-----HHGEDKLPW 337
 OY 275 WGRFPMN--TGDLSTNNMFVALCAFGEGMHN-----HHAFGSARHG 316
 DB 338 YRCKMWSYLRGLTTLDR-----DYGMINNIHHDICTHYIHLFPIPHYH 384
 RESULT 15
 FD3D_ARATH STANDARD; PRT; 435 AA.
 AC P48622;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Temperature-sensitive omega-3 fatty acid desaturase, chloroplast
 DE precursor (EC 1.14.99.-).
 GN FAD8 OR AT5G05580 OR MOP10.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA; TISSUE-Aerial parts;
 RX MEDLINE=95148742; PubMed=7846164;
 RA Gibson S., Arondel V., Ida K., Somerville C.R.;
 RT Cloning of a temperature-regulated gene encoding a chloroplast
 RT omega-3 desaturase from Arabidopsis thaliana.";
 RL Plant Physiol. 106:1615-1621(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA; TISSUE-Hypocotyl;
 RA Wataniki M.C., Yamamoto K.T.;
 RT Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. Columbia;
 RX MEDLINE=97471969; PubMed=9330910;
 RA Sato S., Kotani H., Nakamura Y., Kaneo T., Asamizu E., Fukami M.,
 RA Miyajima N., Tabata S.;
 RT Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
 RT features of the 1.6 Mb regions covered by twenty physically assigned
 RT pl clones.";
 RL DNA Res. 4:215-230(1997).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- INDUCTION: BY LOW TEMPERATURE.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC -----
 DR EMBL: L27158; AA65621.1; -
 DR EMBL: U08216; AAB60302.1; -
 DR EMBL: D17578; BAA04504.1; -
 DR EMBL: AB005241; BAB1547.1; -
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF00487; FA_desaturase; 1.

DR Prodom: PD001081; FA_desaturase; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KM Transil peptidase.
 FT TRANSIT 1
 FT CHAIN 1
 FT FT 435
 FT DOMAIN 156
 FT DOMAIN 192
 FT DOMAIN 359
 SQ SEQUENCE 435 AA; 50136 MW; 3D77A8035A6214E1 CRC64;
 Query Match 4.9%; Score 95.5; DB 1; Length 435;
 Best local Similarity 20.8%; Pred. No. 0.59;
 Matches 75; Conservative 37; Mismatches 104; Indels 145; Gaps 21;
 OY 48 PKTEPKP-KDLEPRITSEVYLERKSKGFWRRKNPRDIONV----- 90
 DB 66 PLFTTQSPSEEDTERFDPCA-----PPFLLADIRAIKHCWVKPMMSSTV 114
 OY 91 --TLVLHLHLMAMPY---FSWDAFWISFILLGFASGVLTLCFHRCTHGF---K 141
 DB 115 YRDVAIVGLAAVAAYFNWMLMPLYWFAQGTMFALFVLG---HDC-GHGSFSDPR 168
 OY 142 LPLVYFFAYCGSLALOGDPMEVSNHRYHQ---FVDEVDVH-----SPTQ 187
 DB 169 LNSVAGHLHSSILVYHG---WLSHRTHQNHGHNDESHPRLPESYKMLEKTTQ 224
 OY 188 GWVF-----CHIGVLDKDLFEYKRGGRNNVNDLKQAFYRF 225
 DB 225 MRFRLPFPMLAYPFYLMNRSPOKOSH--YHPDSDLFPRK-----KKDY 268
 OY 226 LQTYVYHOLA--LIALLYVG-----GPPYIWMGKGFRLVMEFSTRAINSVCHK- 274
 DB 269 LSTINCKTMAALLVCLNFVWGPDIOMLKLYGIPYIFVWMLDFVYLH-----HHG 319
 OY 275 -----WGRFPMN--TGDLSTNNMFVALCAFGEGMHN-----HHAFGSARHG 315
 DB 320 HEDKLPWYRGKMSYLRGLTTLDR-----DYGMINNIHHDICTHYIHLFPIPHYH 372
 OY 316 L 316
 DB 373 L 373

Search completed: September 13, 2002, 11:58:48
 Job time: 7764 sec

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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:47:44 ; Search time 68.94 Seconds
(without alignments)
893.330 Million cell updates/sec

Title: US-09-664-840-2

Perfect score: 1946
Sequence: 1 LRLSLVPPISISLSLEAM.....ATNVKLPTEAKOKLIKAKSA 356Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1940	99.7	356	10	Q9FV68 Limanthus
2	978.5	50.3	371	10	Q9LVZ4 Arabidopsis
3	976.5	50.2	371	10	Q949X0 Arabidopsis
4	887.5	45.6	305	10	Q65797 Arabidopsis
5	874.5	44.9	307	10	Q65798 Arabidopsis
6	870.5	44.7	311	10	Q9SID2 Arabidopsis
7	833	42.8	299	10	Q9LND8 Arabidopsis
8	801	41.2	303	10	Q04700 Rosa hybrid
9	796	40.9	314	10	Q9LVZ3 Arabidopsis
10	792	40.7	299	10	Q9FV65 Arabidopsis
11	788.5	40.5	319	10	Q9LMT4 Arabidopsis
12	786.5	40.4	299	10	Q9LMT3 Arabidopsis
13	775.5	39.9	299	10	Q9LND9 Arabidopsis
14	741	38.1	287	10	Q9LND6 Arabidopsis
15	687	35.3	272	2	Q44502 Anabaena va
16	650	33.4	318	16	Q55406 Synechocyst

17	632.5	32.5	270	2	Q33722 Spirulina p
18	626	32.2	277	2	Q07873 Synechococ
19	595	30.6	279	2	Q9ZAP7 Synechococ
20	556	28.6	278	2	Q44117 Synechococ
21	448	23.0	300	2	Q9R6T6 Synechococ
22	445	22.9	336	2	Q9K3T6 Streptomyce
23	423.5	21.8	479	3	Q94523 Schizosacch
24	407	20.9	555	3	P79078 Cryptococcu
25	402	20.7	493	3	P79077 Cryptococcu
26	384.5	19.8	292	5	Q94824 Tetrahymena
27	369	19.0	476	10	Q80331 Cyanidiosch
28	366.5	18.8	384	5	Q9VFX5 Drosophila
29	362	18.6	452	3	Q13378 Muscor rouxi
30	359.5	18.5	461	5	Q9VA94 Drosophila
31	359	18.4	451	3	P79049 Pichia angu
32	358.5	18.4	339	5	Q01708 Caenorhabdl
33	357.5	18.4	445	3	Q94215 Mortierella
34	355	18.2	445	3	Q9UVW5 Mortierella
35	354	18.2	445	3	Q94214 Mortierella
36	354	18.2	445	3	Q94747 Mortierella
37	352.5	18.1	383	5	Q94541 Drosophila
38	352	18.1	324	13	Q9PW15 Drosophila
39	352	18.1	486	3	Q94036 Candida alb
40	351.5	18.1	383	5	Q9VC66 Drosophila
41	350.5	18.0	292	5	Q15810 Tetrahymena
42	350.5	18.0	383	5	Q9U967 Drosophila
43	349.5	18.0	351	5	Q9NG08 Argyrotaeni
44	349	17.9	355	11	Q9Z216 Mus musculu
45	348.5	17.9	383	5	Q9U972 Drosophila

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	356 AA.
Q9FV68	Q9FV68	Q9FV68		
AC	Q9FV68	Q9FV68		
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	DELTA5 ACYL-CoA DESATURASE (FRAGMENT).			
OS	Limanthus douglasii (Douglas's meadowfoam).			
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Limnathaceae; Limnathes.			
OX	NCBI_TaxId=28973;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20438218; PubMed=10982439;			
RA	Cahoon E.B., Marillia E.F., Stecca K.L., Hall S.E., Taylor D.C.,			
RA	Kluey A.J.;			
RT	"Production of fatty acid components of meadowfoam oil in somatic			
RT	soybean embryos."			
RL	Plant Physiol. 124:243-252(2000).			
DR	EMBL; AF247133; AAG28599.1; -.			
DR	InterPro: IPR001522; Desaturase.			
DR	Pfam: PF01069; Desaturase: 1.			
DR	PRINTS: PR00075; FACDSATRASE.			
DR	ProDom; PD002221; Desaturase: 1.			
FT	NON-TER			
SQ	SEQUENCE 356 AA; 41038 MW; E0CD4BCB8F7B534C CRC64;			
QY	Query Match	99.7%	Score 1940;	DB 10; Length 356;
	Best Local Similarity	99.4%	Pred. No. 5.2e-176;	
	Matches 354; Conservative	2;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 LRLSLVPPISISLSLEAMAFIATTPAMPFASVLDPKITPKPKETPKPKDLE 60			
DB	1 LRLSLVPPISISLSLEAMAFIATTPAMPFASVLDPKITPKPKETPKPKDLE 60			
QY	61 RFTSEVLEKSKGFRKRNPRDIONAVTLVLVLAAMAPPYFSWDAFWISFILGP 120			

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Db 61 RFRSEVLERAKGFMRKMPDIONAVTLVHALAANAFESWDAFWISILLGF 120
Qy 121 ASGVGILTCFHRCLTHGGFKLPKLYEFPAFCGSLALOGDPMENSHNRHNOVDTER 180
Db 121 ASGVGILTCFHRCLTHGGFKLPKLYEFPAFCGSLALOGDPMENSHNRHNOVDTER 180
Qy 181 DVHSEPTGFWFCHIGWLDKDLFEVKEGRRNNNDLKKOAFRFLQKTYMHQALAL 240
Db 181 DVHSEPTGFWFCHIGWLDKDLFEVKEGRRNNNDLKKOAFRFLQKTYMHQALAL 240
Qy 241 LYYGGEFYIWMGGEFLVPMFHSFALNSVCHKMGGRPMNGDSTNNMFALCAGGEG 300
Db 241 LYYGGEFYIWMGGEFLVPMFHSFALNSVCHKMGGRPMNGDSTNNMFALCAGGEG 300
Qy 301 WHNNHAFEGSARHGLEWMOIDVTWYVIRTLQALIGLATNVKLPTEAKOKKLAKSA 356
Db 301 WHNNHAFEGSARHGLEWMOIDVTWYVIRTLQALIGLATNVKLPTEAKOKKLAKSA 356
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RESULT 2
Q9LVZ4 PRELIMINARY; PRT; 371 AA.
ID 09LVZ4
AC 09LVZ4
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE DELTA 9 DESATURASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA.
RA MEDLINE-20277480; PubMed-10819329;
RX Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty p1 and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
DR EMBL: AB017071; BAB02316.1; -.
DR InterPro: IPR001522; Desaturase.
DR Pfam: PF01069; Desaturase.1.
DR PRINTS: PR00075; FACDDSATRASE.
DR PRODOM: PD002221; Desaturase.1.
SQ SEQUENCE 371 AA; 42580 MW; F1D62B9F44795FCC CRC64;
```

Query Match 50.38; Score 978.5; DB 10; Length 371;
Best Local Similarity 56.28; Pred. No. 1.1e-84;
Matches 173; Conservative 52; Mismatches 80; Indels 3; Gaps 3;

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Qy 45 KPEKTEPRKDKDLERRTSEVLERSK-GFMRKKNPPDIONAVTLVHALAAMAP 103
Db 61 KRDTTAAATGEGDYRRIMLSDVLYKKKEKYWVEREKAMPFGAVAVVLSMHLISLAP 120
Qy 104 FYFSMDAFWISFILLGFASGVLTGTCFHRCLTHGGFKLPKLYEFPAFCGSLALOGDPM 163
Db 121 FQFWRAVAVAFGLY-ITYGLIGTILSFHRNLSHKAFLPKWLELYFAFCGALOGNPI 179
Qy 164 EWSNHRHNOFVPTEDVHSPTOGFNEFCHIGWLDKDLFEVKEGRRNNNDLKKOAFY 223
Db 180 DWVSTHRYHNOFCDSDRPHSPDLGFWFESHNNMFDTNT-ITQRCGEENNVGDLEKQPFY 238
Qy 224 RFLQKTYMHQALALALYYGGEFYIWMGGEFLVPMFHSFALNSVCHKMGGRPMNTG 283
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Db 239 RFLRTTYLHPLALAVALYAMGGEFYIWMGGEFLVPMFHSFALNSVCHKMGGRPMNTG 298
Qy 284 DLSTNNMFVALCAGGEGWHNNHAFEGSARHGLEWMOIDVTWYVIRTLQALIGLATNVKLP 343
Db 299 DLSTNNMFVALCAGGEGWHNNHAFEGSARHGLEWMOIDVTWYVIRTLQALIGLATNVKLP 358
Qy 344 TEAKOKKL 351
Db 359 SEAKOKRM 366
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RESULT 3
Q949X0 PRELIMINARY; PRT; 371 AA.
ID 0949X0
AC 0949X0
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE PUTATIVE DELTA 9 DESATURASE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamlya A., Karlin-Neumann G., Kawai J., Kim C., Koeseema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene MSJ1.25/AT3G15850 (GI:11994357).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY050838; AAK92773.1; -.
SQ SEQUENCE 371 AA; 42550 MW; 45C67AD60CE1860D CRC64;
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Query Match 50.28; Score 976.5; DB 10; Length 371;
Best Local Similarity 56.28; Pred. No. 1.7e-84;
Matches 173; Conservative 52; Mismatches 80; Indels 3; Gaps 3;

```
Qy 45 KPEKTEPRKDKDLERRTSEVLERSK-GFMRKKNPPDIONAVTLVHALAAMAP 103
Db 61 KRDTTAAATGEGDYRRIMLSDVLYKKKEKYWVEREKAMPFGAVAVVLSMHLISLAP 120
Qy 104 FYFSMDAFWISFILLGFASGVLTGTCFHRCLTHGGFKLPKLYEFPAFCGSLALOGDPM 163
Db 121 FQFWRAVAVAFGLY-ITYGLIGTILSFHRNLSHKAFLPKWLELYFAFCGALOGNPI 179
Qy 164 EWSNHRHNOFVPTEDVHSPTOGFNEFCHIGWLDKDLFEVKEGRRNNNDLKKOAFY 223
Db 180 DWVSTHRYHNOFCDSDRPHSPDLGFWFESHNNMFDTNT-ITQRCGEENNVGDLEKQPFY 238
Qy 224 RFLQKTYMHQALALALYYGGEFYIWMGGEFLVPMFHSFALNSVCHKMGGRPMNTG 283
Db 239 RFLRTTYLHPLALAVALYAMGGEFYIWMGGEFLVPMFHSFALNSVCHKMGGRPMNTG 298
Qy 284 DLSTNNMFVALCAGGEGWHNNHAFEGSARHGLEWMOIDVTWYVIRTLQALIGLATNVKLP 343
Db 299 DLSTNNMFVALCAGGEGWHNNHAFEGSARHGLEWMOIDVTWYVIRTLQALIGLATNVKLP 358
Qy 344 TEAKOKKL 351
Db 359 SEAKOKRM 366
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RESULT 4
ID 065797 PRELIMINARY; PRT; 305 AA.
AC 065797;

DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-DEC-1998 (TReMBLrel. 19, Last sequence update)
 DE DELTA 9 DESATURASE (T21E18.13 PROTEIN) (PUTATIVE DESATURASE
 DE PROTEIN).
 GN ADS1 OR T21E18.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98220322; PubMed=9559566;
 RA Fukuchi-Mizutani M., Tasaka Y., Tanaka Y., Ashikari T., Kusumi T.,
 RA Murata N.;
 RT "Characterization of delta 9 acyl-11lipid desaturase homologues from
 RT Arabidopsis thaliana."
 RL Plant Cell Physiol. 39:247-253(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Sakano H., Vayberg M., Lee J., Lenz C., Liu S.X., Pham P.,
 RA Toriumi M., Yu G., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
 RA Hong B., Liu A., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shin P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federapfel N.A., Theologis A.;
 RT "The sequence of BAC T21E18 from Arabidopsis thaliana chromosome 1.";
 RN Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Eguu P., Lee J.M.,
 RA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
 RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shin P.,
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene T21E18.13 (GI:8810470)."
 RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: DB8536; BAA25180.1; -;
 DR EMBL: AC024174; AAF80131.1; -;
 DR EMBL: AF33433; AAG48796.1; -;
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR Prodom: PD002221; Desaturase; 1.
 SO SEQUENCE 305 AA, 36106 MW, 10BDABE2162AFC2D0 CRC64;

Query Match 45.6%; Score 887.5; DB 10; Length 305;
 Best Local Similarity 51.4%; Pred. No. 3.9e-76;
 Matches 152; Conservative 53; Mismatches 88; Indels 3; Gaps 2;

OY 56 KDLERFRTSEVYLERKSKGFRKRNPNIDIONAVTLVLHALLAMAPYFSMDATWISF 115
 DB 9 EENNKKMAADKEMGKRRKAMMERKRLDIYKAFASLVEHFLCLLAPNFTPALRALVAL 68
 OY 116 ILGFAVGLITLCEFHRCITLHGFGFKLPKLYEYFAYCGSLALOGDPMEWYSHRYNHOF 175
 DB 69 IV--YVGGIGITVSYHRLNARSEKVPKWELEFFAYCGSLALOGDPIDWSTHRYNHOF 126
 OY 176 VTERDVHSPGTFWCHIGWVLDKDLFEYKRGGRNNVNDLKKAFYRFLQTYKHOL 235
 DB 127 TDSDRPHSPNEGFWFSHLLMLEDGTLYEK--CGRTVNEDELKROYUYFLDQTVLXHL 185
 OY 236 ALIALLYYGGFRYYIWMGFRFLVFHFSTPAINSCHWKGGRPNWTGDLSTNNMFALC 295
 DB 186 TFGFLYYGGISFLTWGNGIGVAMEIHVTCILNSCHWGSTWKTNTDSRYVWMLSYF 245
 OY 296 AFGEGHNNHNAFEOSARHGLEWMOIDVTWYIRTLQALIGLATNVKLPTEAKOKL 351
 DB 246 SFGESNNHNNHNAFESSAROGLEWMOIDISWYIRFLEITGLATDVKLPESORRRM 301

RESULT 5

065798
 ID 065798 PRELIMINARY; PRT; 307 AA.
 AC 065798;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-DEC-1998 (TReMBLrel. 19, Last sequence update)
 DE DELTA 9 DESATURASE (PUTATIVE DELTA 9 DESATURASE).
 GN ADS2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98220322; PubMed=9559566;
 RA Fukuchi-Mizutani M., Tasaka Y., Tanaka Y., Ashikari T., Kusumi T.,
 RA Murata N.;
 RT "Characterization of delta9 acyl-11lipid desaturase homologues from
 RT Arabidopsis thaliana."
 RL Plant Cell Physiol. 39:247-253(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
 RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M.,
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamuya A., Karlin-Neumann G.,
 RA Kawai J., Kim C., Kosemura E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
 RA Shin P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
 RA Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene T28P16.15/At2g31360 (GI:4589964)."
 RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: DB8537; BAA25181.1; -;
 DR EMBL: AY045918; AKK76592.1; -;
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR Prodom: PD002221; Desaturase; 1.
 SO SEQUENCE 307 AA, 36375 MW, 8E26FA0F2E9EEAEB CRC64;

Query Match 44.9%; Score 874.5; DB 10; Length 307;
 Best Local Similarity 52.4%; Pred. No. 6.7e-75;
 Matches 152; Conservative 46; Mismatches 87; Indels 5; Gaps 3;

OY 64 TSEVYLERKSKG--FWRRKRNPNIDIONAVTLVLHALLAMAPYFSMDATWISF 121
 DB 17 TPAVVEKKRRKRVNFWDRKRRRLDYKFSASFVHSLALAPFTWSALWTFLE--YT 74
 OY 122 SGVLGTTLCFHRCLNHGFKLPKLYEYFAYCGSLALOGDPMEWYSHRYNHOFVTERD 181
 DB 75 IGGIGITVSYHRLNARSEKVPKWELEFLAYCALALIQGDPIDWSTHRYNHOFQTSERD 134
 OY 182 VHSPTGFWFCHIGWVLDKDLFEYKRGGRNNVNDLKKAFYRFLQTYKHOLALIAL 241
 DB 135 PHSPEKGFWSHLLMLEDGTLYEYK--CGRANVEDLKRWFYRFLQTYKHOLALIAL 193
 OY 242 YVGGFRYYIWMGFRFLVFHFSTPAINSCHWKGGRPNWTGDLSTNNMFALCARGEGM 301
 DB 194 FYLGMSFYTWGMGVALEHVHTCLNSCHWKGRTKKTNDISNNWMLSVSFGESW 253
 OY 302 HNNHNAFEOSARHGLEWMOIDVTWYIRTLQALIGLATNVKLPTEAKOKL 351
 DB 254 HNNHNAFESSAROGLEWMOIDISWYIRFLEITGLATDVKLPTEAKORRRM 303

RESULT 6
 O9SID2
 ID 09SID2 PRELIMINARY; PRT; 311 AA.
 AC 09SID2;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE DELTA 9 DESATURASE.
OS AR2G31360.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_COLUMBIA;
EX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shree T.P., Benito M.-T., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buelli C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vankken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.,
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RT Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_COLUMBIA.
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007169; AAD26482.1; -
DR InterPro: IPR001522; Desaturase.
DR Pfam: PF01069; Desaturase; 1.
DR PRINTS: PR00075; FADCDSATRASE.
DR ProDom: PD002221; Desaturase; 1.
SQ SEQUENCE 311 AA; 36848 MW; A6F5337E186BCF79 CRC64;

Query Match 44.7%; Score 870.5; DB 10; Length 311;
Best Local Similarity 51.9%; Pred. No. 1.6e-74;
Matches 152; Conservative 46; Mismatches 88; Indels 7; Gaps

RN SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA:
 RA Sakano H., Vaysberg M., Lee J., Lenz C., Liu S.X., Pham P.,
 RA Toriumi M., Yu G., Chiu C., Chlou J., Choi E., Chung M., Gonzalez A.,
 RA Howng B., Liu A., Altai H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;
 RT "The sequence of BAC T2LE18 from *Arabidopsis thaliana* chromosome 1.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC024174; AAF80133.1; -
 DR InterPro; IPR001522; Desaturase.
 DR Pfam; PF01069; Desaturase; 1.
 DR PRINTS; PR00075; FACDDSATRASE.
 DR Prodom; PD002221; Desaturase; 1.
 SQ SEQUENCE 299 AA; 35355 MW; 9FCDBA8CF21D6507 CRC64;

 Query Match 42.8%; Score 833; DB 10; Length 299;
 Best Local Similarity 51.7%; Pred. No. 5,6e-71;
 Matches 153; Conservative 47; Mismatches 90; Indels 6; Gaps 3;

 QY 56 KDDLERFRTSEVLEERKKGFMRKRNDRDIONMTLLVLAHALAMAFYSPDAFISF 115
 DB 6 KDDGSSQKRS--VRKEKRAYLVRKWTFDPDGRASTVTHLLCLLAFNNKWEFRFGCI 62
 QY 116 ILLEGASVGLITLGFHRCITLTHGFEKPLKIVEFYFAYCGSLALOGDPMEWYSNHRVHOF 175
 DB 63 ILALITN--LCITTFYHNNLTTHRSFKLEPKWLEYPAYGALLALOGDPIDWYSIHFRHQF 120
 QY 176 VDTEEDVNSPIPOGFHFCIGVWLKDLFEVRRGGRNNVNDLKAQAFRFLQKTYMQL 235
 DB 121 TQSDSDPHSPLEGFEFHSVLIIFPDV-YIRKRCGRNNVMDLKQWFRFLKTVLIL 179
 QY 236 ALIALVYVGEPFYVWCGFRLVFMFSTALINSCVCHKMGGRPNMTDLSNNMFALC 295
 DB 180 AFWLITLIMGGFPLVITWVGVGFGVIGCHTMYVNSACHICSGQAMQINDTSRWVWALL 239
 QY 296 AFEGEWHNNHAFEOSARHGLEWMOIDVTWYIRFLQALIGLATNKKLPTFAOKRL 351
 DB 240 TMGESWHNNHAFETSARHGLEWOLDITWYLIWFFOALGLATNKKLPTDOKRKM 295

 RESULT 8
 ID 004700 PRELIMINARY; PRT; 303 AA.
 AC 004700;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE DELTA-9 DESATURASE (FRAGMENT).
 OS Rosa hybrid cultivar.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Rosales; Rosaceae; Rosoideae; Rosa.
 CC NCBI_Taxid=128735;
 CX [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=96128006; Pubmed=8541490;
 RA Fukuchi-Mizutani M., Savin K., Cornish E., Tanaka Y., Ashikari T.,
 RA Kusumi T., Murata N.;
 RT "Senescence-induced expression of a homologue of delta 9 desaturase in
 rose petals.";
 RL Plant Mol. Biol. 29:627-635(1995).
 RN [2]
 RP SEQUENCE OF 7-303 FROM N.A.
 RC STRAIN-KARDINAL; TISSUE-PETAL;
 RA Nishida I.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; S80863; AAB50679.1; -
 DR EMBL; D49385; BAA23136.1; -
 DR EMBL; D49383; BAA23134.1; -

OY 294 LCAGEGHHNNHAFESARHGLEWMOIDVTWYVIRTLQALATNVLKLPTEAOKKL 351
 DB 238 PFTMGESHHNNHAFESARHGLEWMOIDVTWYVIRTLQALATNVLKLPTEAOKRKM 295

RESULT 11

O9LMT4 PRELIMINARY; PRT; 319 AA.

AC O9LMT4; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE T2D23.5 PROTEIN.
 GN T2D23.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;

SEQUENCE FROM N.A.

RA STRAIN-CV, COLUMBIA;

RA Liu S.X., Vaysberg M., Etgu P., Lee J.M., Lenz C., Pham P., Sakano H.,
 Toriumi M., Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A.,
 Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 Federici N.A., Theologis A.;
 RA "The sequence of BAC T2D23 from Arabidopsis thaliana chromosome 1.";
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC068143; AF82163.1; -
 DR InterPro; IPR001522; Desaturase.
 DR Pfam; PF01069; Desaturase; 1.
 DR PRINTS; PR00075; FACDDSATRASE.
 DR ProDom; PD002221; Desaturase; 1.

DR PRODOM; PD002221; Desaturase; 1.
 SQ SEQUENCE 319 AA; 37455 MW; 82377E95153550A2 CRC64;

Query Match 40.5%; Score 788.5; DB 10; Length 319;
 Best Local Similarity 50.2%; Pred. No. 1e-66;

Matches 144; Conservative 46; Mismatches 94; Indels 3; Gaps 2;

OY 65 SEVLEKSKGFWRKRNPRDIONAVTLVLAALAAAFYFSMDAFISFLLGFASGV 124
 DB 32 SRVSTMQKRAVYFOROMPLVDVVASVYVIVHFLCLAPFNKWEA--LRGLVIFALTT 89
 OY 125 LGILCFRCLTHGGFKLPKLYEFYFACGSLAGDPMEMVSNHRYHNOVDTERVHS 184
 DB 90 LSTFSEHRLNLSHSEFKLPKLETPMAVSAYFAVLAQGDPMVSIHREHNOFTSDRDPS 149
 OY 185 PTOGFWECHIGVLDKDLFEKRGGRNNVNDLKKQAFYRFLQKTYMHQALALALYYV 244
 DB 150 PKBGLFSLIMIFDQYIKKCGG-RDNVLDLKKQWFKYKRLRTIAVHILMEFTILXY 208
 OY 245 GGFYIWMGKFLVFMFHSFPAINSVCHKMGGRPWNTGDLSTNNMFALCAFGEGHHNN 304
 DB 209 GGLPYLRCGGVGFIFIGYHVLVNSACHIMGSRSMWTKDTSRRVWMLSTFTMGESHHNN 268
 OY 305 HHAFESARHGLEWMOIDVTWYVIRTLQALATNVLKLPTEAOKKL 351
 DB 269 HHAFESARHGLEWMOIDVTWYVIRTLQALATNVLKLPTEAOKKL 315

RESULT 12

O9LMT3 PRELIMINARY; PRT; 299 AA.

AC O9LMT3; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE T2D23.6 PROTEIN (PUTATIVE DELTA 9 DESATURASE PROTEIN).
 GN T2D23.6.
 OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;

SEQUENCE FROM N.A.

RA STRAIN-CV, COLUMBIA;

RA Liu S.X., Vaysberg M., Etgu P., Lee J.M., Lenz C., Pham P., Sakano H.,
 Toriumi M., Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A.,
 Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 Federici N.A., Theologis A.;
 RA "The sequence of BAC T2D23 from Arabidopsis thaliana chromosome 1.";
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC068143; AF82164.1; -
 DR InterPro; IPR001522; Desaturase.
 DR Pfam; PF01069; Desaturase; 1.
 DR PRINTS; PR00075; FACDDSATRASE.
 DR ProDom; PD002221; Desaturase; 1.

DR PRODOM; PD002221; Desaturase; 1.
 SQ SEQUENCE 299 AA; 35510 MW; 9682DBF5BA46E35D CRC64;

Query Match 40.4%; Score 786.5; DB 10; Length 299;
 Best Local Similarity 50.5%; Pred. No. 1.e-66;

Matches 143; Conservative 42; Mismatches 95; Indels 3; Gaps 2;

OY 69 LEKSKGFWRKRNPRDIONAVTLVLAALAAAFYFSMDAFISFLLGFASGVGIT 128
 DB 16 VSKKRPYIHHEMSWADIIRALTYINVHFLCLAPFNKWEALRFGVLAALS--LST 73
 OY 129 LCFRCLTHGGFKLPKLYEFYFACGSLAGDPMEMVSNHRYHNOVDTERVHSPTG 188
 DB 74 FSYHRLNLSHSEFKLPKLETPMAVSAYFAVLAQGDPMVSIHREHNOFTSDRDPSIEG 133
 OY 189 FWFCHIGVLDKDLFEKRGGRNNVNDLKKQAFYRFLQKTYMHQALALALYYVGF 248
 DB 134 FWFCHIGVLDKDLFEKRGGRNNVNDLKKQAFYRFLQKTYMHQALALALYYVGF 192
 OY 249 YIWMGKFLVFMFHSFPAINSVCHKMGGRPWNTGDLSTNNMFALCAFGEGHHNNHAF 308
 DB 193 YLTCGGVGVIGYHVLVNSACHIMGSRSMWTKDTSRRVWMLSTFTMGESHHNNHAF 252
 OY 309 EGSARHGLEWMOIDVTWYVIRTLQALATNVLKLPTEAOKKL 351
 DB 253 ESSARHGLEWMOIDVTWYVIRTLQALATNVLKLPTEAOKKL 295

RESULT 13

O9LND9 PRELIMINARY; PRT; 299 AA.

AC O9LND9; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE T2IE18.14 PROTEIN.
 GN T2IE18.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;

RC STRAIN-CV, COLUMBIA:
 RA Sakano H., Vayenberg M., Lee J., Lenz C., Liu S.X., Pham P.,
 RA Tortum M., Yu G., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
 RA Hong B., Liu A., Altai H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;
 RT "The sequence of BAC T21E18 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024174; AAF80132.1;
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FACDSATURASE.
 DR Prodom: PD002221; Desaturase; 1.
 SQ SEQUENCE 299 AA; 34769 MW; 4640982a38CA9E46 CRC64;

Query Match 39.9%; Score 775.5; DB 10; Length 299;
 Best Local Similarity 51.8%; Pred. No. 1.6e-65;
 Matches 145; Conservative 37; Mismatches 95; Indels 3; Gaps 2;

OY 72 KSKFMRKRNPRDIONAVTLVLHALLAAMAPFYSWDAFWISFLLGFASGVLTICF 131
 DB 19 EKRAFFERKWTRIDIAASAVGAVHLLCLAFENYKWEALRFGVILATVTS--LSIFSY 76
 OY 132 HRCITGGFKLPKLYEFYFVCGSLALQDPMENVNHRHYHOVTERDVHSPTQGFWR 191
 DB 77 HRLTIHSFPLKPLEFPFAYSALEFALQGHPTDWSHTRHDPDSDRPHSPITGFWF 136
 OY 192 CHIGWVLQDLFEKRGRRNNVNDLKKQAFYFLQKTYMHOLALIALIYYGGFPIYV 251
 DB 137 SHVFWIDTSTYIREKCGG-RDNYVDLQKQWYFRLNTIGLITLFWTLVYLMGGLPYLR 195
 OY 252 MCGMFRLVFHFSTFALNSYCHMGCPWNTGDLSTNNMVALCAGEGHHNNHAFEOS 311
 DB 196 CGVGVGGTITNGTLWLSACHITGSSRAMWTKTSRTINWLGPTMGESWHNNHAFES 255
 OY 312 ARHGLEWQIDVTWYVIRTLQALIGLATNVKLPTEAOKRL 351
 DB 256 ARHGLEWYQVDLWYLLCFQALGIANVDVLTPTDAOKRL 295

RESULT 14
 O9LND6 PRELIMINARY; PRT; 287 AA.
 AC O9LND6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE T21E18.17 PROTEIN.
 GN T21E18.17.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotyle II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA:
 RA Sakano H., Vayenberg M., Lee J., Lenz C., Liu S.X., Pham P.,
 RA Tortum M., Yu G., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
 RA Hong B., Liu A., Altai H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federspiel N.A., Theologis A.;
 RT "The sequence of BAC T21E18 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024174; AAF80135.1;
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FACDSATURASE.
 DR Prodom: PD002221; Desaturase; 1.
 SQ SEQUENCE 287 AA; 33565 MW; 6F491EF9733F6201F CRC64;

Query Match 38.1%; Score 741; DB 10; Length 287;
 Best Local Similarity 47.0%; Pred. No. 2.9e-62;
 Matches 140; Conservative 44; Mismatches 96; Indels 18; Gaps 5;

OY 54 KPRDLEERTSEVLEKSKGFWRRKRNPRDIONAVTLVLHALLAAMAPFYSWDAFWI 113
 DB 4 KNRDSS---SQKAVRKEKRAFLFKRWTRVDYMRASAVGAVHLLCLAFENYKWEALRFGVILATVTS--LSIFSY 76
 OY 114 SFLLGFASGVLTICFPHRCLTHGFKLPKLYEFYFVCGSLALQDPMENVNHRHYH 173
 DB 61 A-AMVGISTN-LSITFSYHNLTHRSFKLPKLYEPFAYSALEFALQGHPTDWSHTRH 118
 OY 174 QFVTERDVHSPNPGFMPFICIGWVLQDLFEKRGRRNNVNDLKKQAFYFLQKTYMH 233
 DB 119 QFTDSDRDHPSPLEGFWFSTFVFWIPTSTYIREKCGG-RDNYVDLQKQWYFRLNTIGLH 177
 OY 234 QALIALIYYGGFPIYVGMGFRLVFMFSTFALNSYCHMGCPWNTGDLSTNNMFA 293
 DB 178 ILTFWILVYLMGGLPYLTWSVGAGALGYHATWLSACHINGSRAMNTKTSRTINWLG 237
 OY 294 LCAFEGSWNNHNAFEOASARHGLEWQIDVTWYVIRTLQALIGLATNVKLPTEAOKRL 351
 DB 238 PFTMGESWHNNHAFESARHGLEWYQV-----LGLATVDVLTPTDAOKRL 283

RESULT 15
 O44502 PRELIMINARY; PRT; 272 AA.
 AC O44502;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FATTY-ACID DESATURASE.
 GN DESC.
 OS Anabaena variabilis.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_Taxid=1172;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95014360; PubMed=7929259;
 RA Sakamoto T., Wada H., Nishida I., Oimori M., Murata N.;
 RT "Delta 9 acyl-lipid desaturases of cyanobacteria. Molecular cloning
 RT and substrate specificities in terms of fatty acids, sn-positions, and
 RT polar head groups.";
 RL J. Biol. Chem. 269:25576-25580(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94207189; PubMed=8155683;
 RA Sakamoto T., Wada H., Nishida I., Oimori M., Murata N.;
 RT "Identification of conserved domains in the delta 12 desaturases of
 RT cyanobacteria.";
 RL Plant Mol. Biol. 24:643-650(1994).
 DR EMBL: D14581; BAA03434.1;
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FACDSATURASE.
 DR Prodom: PD002221; Desaturase; 1.
 SQ SEQUENCE 272 AA; 31418 MW; E2FBD0CB490D0696 CRC64;

Query Match 35.3%; Score 687; DB 2; Length 272;
 Best Local Similarity 47.6%; Pred. No. 3.7e-57;
 Matches 128; Conservative 48; Mismatches 73; Indels 20; Gaps 4;

OY 88 NAVTLVLVH--ALAAAMPFYSWDAFWISFLLGFASGVLTICFPHRCLTHGFKLPKL 145
 DB 15 NTLFGLGHIALALPAFIPSNFSAAGVA-LLLWITGGLGITLGFRLVTHRSFQTPKW 73
 OY 146 VEYFPAVCGSLALQDPMENVNHRHYHOVTERDVHSPTQGFHICIGWV----- 198
 DB 74 LEYFLVLCGTIACGGPLEWVGTHRIHLSHSDTDPDPDHSNKGKFWMSHIGMLIYHSFSA 133

